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Listing first 45 summaries
September 5, 2002, 02:57:10; Search time 3627.71 Seconds (without alignments) 13334.331 Million cell updates/sec
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     A1089319 qb16d05.x
A1805323 te32h05.x
B6611610 602613533
AA122079 zk93g10.s
AA495807 zw05c04.s
A1682875 wc69d11.x
BF191498 239107 MA
AQ595136 HS_5424_B
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AQ74559 HS_2275-A
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RESULT BB665906 LOCUS DEFINITION

ALIGNMENTS

EST 26-OCT-2001 adult female

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628) Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashiaki, Y. NIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001) BB665906 BB665906.1 GI:16499539 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus BB665906 RIKEN full-length enriched, 2 days pregnant adult fee ovidect Mus musculus cDNA clone E230022G02 5', mRNA sequence. house mouse.

REFERENCE AUTHORS

TITLE

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

CONTRACT	Onto the Court
COMMENT	יייייייייייייייייייייייייייייייייייייי
	Laboratory for Genome Exploration Research Group, RIKEN Genomic
	Sciences Center(GSC), Yokohama Institute
	The Institute of Physical and Chemical Research (RIKEN)
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
	Tel: 81-45-503-9222
	Fax: 81-45-503-9216
	<pre>Email: genome-res@gsc.riken.go.jp,</pre>
	<pre>URL:http://genome.gsc.riken.go.jp/</pre>
	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
	,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
	Normalization and subtraction of cap-trapper-selected cDNAs to
	prepare full-length cDNA libraries for rapid discovery of new
	genes. Genome Res 10 (10), 1617-1630 (2000)
	wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
	Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
	,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
	Hayashizaki, Y.

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AQ745959 AQ053279 AA626188

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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adult female oviduct"
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/dev_stage="2 days pregnant adult"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/note="site_1: SalI; Site_2: BamHI; cDNA library was
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qb16d05.x1 Soares_pregnant_uterus_NbHPU
IMAGE:1696425 3', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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This clone is available royalty-free through LLNL ; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: -40ml3 fwd. ET from Amersham
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                                                                                                                                                                                                 /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
oligo(dT) primer {5'
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1696425"
                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                          12.1%;
                                                                                                          0,
                                                                                                                          Score 433.8; DB 9; Pred. No. 5.8e-75;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ph.D.
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AI805323/c
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                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI805323 444 bp 1
te32h05.xl Soares_NFL_T_GBC_S1 Homo
IMAGE:2087673 3', mRNA sequence.
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AI805323.1 GI:5391889
                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              140
                                                                                                                                                                                                                                                                                            quality sequence stop: 437
          /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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              Ø
                                                                                                                                                                                           /clone="IMAGE:2087673"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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602613533F1 NIH_MGC_60 Homo sapiens
                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1609 row: a column: 10
High quality sequence stop: 602.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 606)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BG611610
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                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
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/db_xref="taxon:9606"
/clone="IMAGE:4738833"
/clone_1ib="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                   /organism="Homo sapiens"
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Primates;
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Pred. No. 2.5e-72;
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                                                                                                                                                                                                                                                                                                                                                                                  GACTAAATTCTCTTATTCTCTTAGTCCTGATGAATAACGTCCTCACCCGTTTACCTGATA 488
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                                                               AA122079 454 bp mRNA
Zk93910.s1 Soares_pregnant_uterus_NbHPU
IMAGE:490434 3', mRNA sequence.
AA122079
AA122079.1 GI:1678117
EST.
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGGGCCAGAGGGGGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NHH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library."
a 131 c
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Chordata;
Primates;
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Pred. No. 1.4e-71;
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Craniata; Vertebrata;
Catarrhini; Hominidae
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                  Euteleostomi;
                                                                                                                                                          EST 19-NOV-1996
                                                                                                                                        cDNA clone
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                                                                                               acctttaagcaggagaagaaatgttttcagatagtttcaaatacnccaaaaatgtttgc 3510
                                                                                                                                                          taactagttgttcttctctagtctctacgttattagnattttttgctttcataatgtgaa
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                                                                                                                                                                                                                                                                          gaacttaatttcaggaaggaaaggtctgtatgtacacatttcactttaagcagaaaatct 3330
tgttctgaaa
                                                                                   ACCTTTAAGCAGGAGAAGCANATGTTNTCAGNTAGTTTCANATACNCCNAAAATGTTTGA
                                                                                                                                           TAACTAGTTGTTCTTCTCTAGTCTCTACGTTATTNGAATTTTNTGCTNTCATAATGTGNA
                                                                                                                                                                                                    TTCTTCAAGAAATGACTTTACTTTTCTCTTTGCACTGCCAGCACGTGAGATACTAACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest park Parkway, Box 8501, St. Louis, MO 63
Tel: 314 286 1800
Fax: 314 286 1810
Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further is
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 454)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., I.
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E.,,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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Contact: Wilson RK
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 405; DB 9;
Pred. No. 2.6e-69;
0; Mismatches 21
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cDNA was primed
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ed with a Not I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
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Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_1: Ecor RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_NhHMPu_S1"
/tlssue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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97.9%;
                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                   Score 404.2; DB 9
Pred. No. 3.7e-69;
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                                                                                                            382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
LNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorthum/LLNL at:
www.blo.llnl.gov/bbrp/image/image.html
Insert Length: 2559 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 413)
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                                                                                                                                                                                                                     140
                                                                                                          Conservative
                                                                                                                                                                                                                                /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Site_2: Not1; Cloned unidirectionally. Primer: Oligc Average insert size 1.72 kb. Life Technologies catal 11548-013"
                                                                                                                                                                                                                                                                                                      /clone="IMAGE:323893"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                           10.3%;
98.2%;
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                                                                                                          Score 369.8; DB 9;
Pred. No. 2.1e-62;
0; Mismatches 6;
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   438;
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239107 MARC
BF191498
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 567)
Pahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Bennett,G.A.,
                                                                                                                                                                                        Plate:
Seq pri
                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
v0.980904.e. Vector identified by cro
                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal PO Box 166, Clay Center, h Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 2:
                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                             stone,R.T., Heaton,M.P.,
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF191498.1
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           Similarity
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                                                                  157
  Conservative
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                                                                                                         /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                  endometrium,
131 c
                                                                /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
131 c 131 g 148 t
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scrofa c
 Score 335.6;
Pred. No. 1e-5
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Grosse,W.M., Bennet
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Teax: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ595136 544 bp DNA linear GSS 08-JUN HS_5424_Bl_E06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1000 Col=11 Row=J, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 544) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. ai
                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC,
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RESULT 10
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (Dases 1 to 286)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                             286
tc10b12.x1 Soares_NhHMPu_S1 H
3', mRNA sequence.
AI375172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1000 Col=11 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
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Pred. No. 1.1e-44;
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                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                               aaattaatttataataatagctaagataaatattttacaaggacatg 2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail nih.gov
This clone is available royalty-free th
IMAGE Consortium (infoeimage.llnl.gov)
Insert Length: 651 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 276.
Location/Qualifiers
                                                                                                                                                              вв635922
вв635922
 Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Roden
1 (bases 1 to 736)
Arakawa,T., Carninci,P.,
                                                                                                                              musculus
BB635922
                                                               Mus musculus
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Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                  вв635922.1
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                                                                                   nouse mouse
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Similarity 99.7%;
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                                                                                                                                             736 bp mRNA linear
RIKEN full-length enriched, 0 day neonat
cDNA clone A430090H24 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and ss clircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mixed (see below); Vector:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2063423"
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                                                                                                                  GI:16471894
                                 Chordata;
Rodentia;
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Pred. No. 7.9e-44;
0; Mismatches 0
   Fukuda,S.,
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                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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ed, 0 day neonate t
   Furuno, M.,
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7) for further
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Hanagaki,T., Hara,A
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer based methods for the mouse full-length cDNA
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Project of Genome Exploration Research Group in Riken
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homc 1 (bases 1 to 292)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., F., Kifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
          Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                   AA122078 292 bp mRNA zk93g10.rl Soares_pregnant_uterus_NbHPU IMAGE:490434 5', mRNA sequence.
AA122078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-499479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pregnant uterus"
/lab_host="DH10B"
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/tlssue_type="Pooled human melanocyte, fetal heart,
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                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                Louis,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTTCCTGCCCAGTTTTCTCTTTTGCTTTAAATGAACATCATCATANGGAATTGGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTTTTAAGAATCCATCTTAACCTCTCTTTAAGTTTCCATACACTTGAGAGCCAACACA 122
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 786)
                                                                                                                                                                                                                 AQ745959
AQ745959.1 GI:5523481
GSS.
                                                                                                                                                                                                                                                                      AQ745959 786 bp
HS_2275_Al_G05_T7C CIT Approved I
sapiens genomic clone Plate=2275
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                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                            Homo sapiens
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Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

a 52 c 51 g 92 t 3 others
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Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
aacTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTT 3'],
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/clone_lib="Soares_pregnant_uterus_NbHPU"
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/lab_host="DH10B"
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/db_xref="GDB:3805021"
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95.9%;
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Primates;
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Pred. No. 4.8e-37;
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5 Col=9
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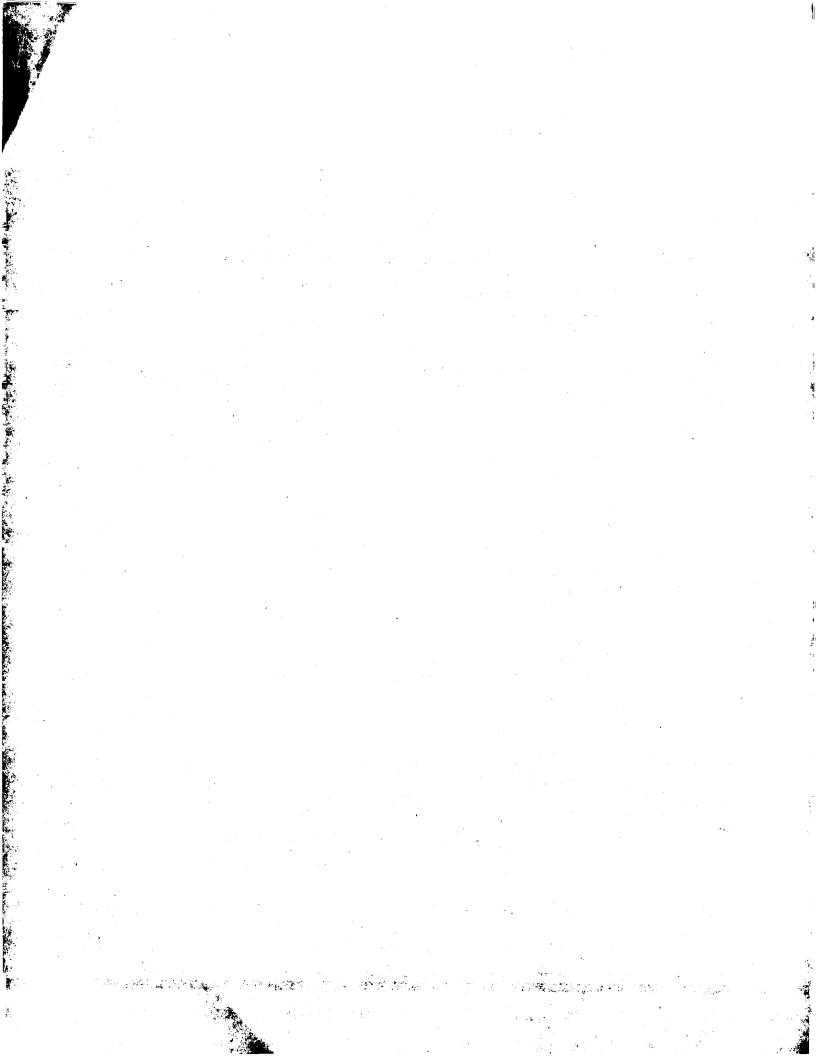
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REFERENCE
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AQ053279.1
                                                                    1 (bases 1 to 593)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bas
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C.,
Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends
High quality sequence stop: 786.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics
BAC end Web Server: http://www.htsc.washington.
Plate: 2275 row: M column: 9
Seq primer: T7
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Contact: Mahairas GG, Wallace JC, Hood Contact: Mahairas GG, Wallace JC, Hood High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle,
             Unpublished (1998)
Other_GSSs: CIT-HSP-2341E13.TR
                                                                                                                                                                                                                                       AQ053279
CIT-HSP-2341E13.TF
                                                     Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                          Building (1998)
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Mark Adams
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E-Coli DH10B"
1 129 c 127 g 239 t
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/db_xref="taxon:9606"
/clone="Plate=2275 Col=9
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/sex="male"
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93.5%;
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F CIT-HSP Hon
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Pred. No. 3.9e-36;
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                                                                                 Bass,S., Linher,K.,
C., Shizuya,H.,
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ne 2341E13, DNA
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Local Similarity 92.0%;
hes 242; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq_primer: M13-21 Class: BAC ends.
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Clones are available from Research
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                        HindIII"
a 112 c
                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2341E13"
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Perfect score:
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1: gb_ba:*
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ALIGNMENTS

AF190500
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DEFINITION
Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7) mRNA, complete cds.
ACCESSION
AF190500
VERSION
AF190500.1 GI:10441729
KEYWORDS
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
HSU, S.Y., Kudo, M., Chen, T., Nakabayashi, K., Bhalla, A., van der Spek, P.J., van Din, M. and Hsueh, A.J.
TITLE
The three subfamilies of leucine-rich repeat-containing G protein-coupled receptors (LGR): identification of LGR6 and LGR7
MOILNE
POURNAL
MEDILINE
2038592
REFERENCE
2 (bases 1 to 2274)
AUTHORS
Hsu, S.Y. and Hsueh, A.J.
Well-REFERENCE
2 (bases 1 to 2274)
AUTHORS
Hsu, S.Y. and Hsueh, A.J.

NOIL Endocrinol. 14 (8), 1257-1271 (2000)
REFERENCE
2 (bases 1 to 2274)
AUTHORS
Hsu, S.Y. and Hsueh, A.J.W.

Qy 499 Db 481	Qy 439 Db 421	Qy 379 Db 361	Qy 324 рb 301	Qy 311 Db 241	Qy 304 a	Qy 244 : Db 121 :	Qy 184 of the first term of th	Qy 124 of Db 1 i	Query Match Best Local : Matches 215	JOURNAL, FEATURES SOUTCE gene CDS CDS
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 Center: Washington University Genome
Center code: WUGSC
Web site:http://genome.wustl.edu/qsc/
                                                                                         Direct Submission
Submitted (16-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 24, 2002 this sequence version replaced gi:18250164.
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AC107219.3 GI:18308921
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Mammalia; Eutheria; Primates;
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Waterston, R.H.
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182907 bases at least Q40
Consensus quality: 183613 bases at least Q30
Consensus quality: 184039 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 186189; sum-of-contigs
Quality coverage: 6.88 in Q20 bases; agarose-fp
Quality coverage: 7.47 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0575B04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 0% Sequencing vector: plasmid; 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
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                   /note="assembly_name:Contig7"
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175874. .178033
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CACTTGAGAGCCCAACACATATTTATTACTAAAAAGATGCTTTGCTAGAAACTCAAAA
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                                                                                        gttcctagtttaaagtagagctttacctgtcatgtgcatcagcaagaatcataggcactt
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Sequence
AX128507
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1191)
Vogeli,G., Wood,L.S. and Merchant,K. gprotein-coupled receptors expressed in brain Patent: WO 0131014 A 15 03-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)
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                                                                                                            human
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/note="unnamed protein pr
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                                            Location/Qualifiers
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WO0131014.
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AAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCATTATGCTGG
                                                      ATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAA
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RGKCRTITVLLIWITGFIVAFIPLSNKEFFKNYYGTNGVCPPLHSEDTESIGAQIY
SVAIFLGINLAAFIIVESYGSMFYSVHQSAITATEIRNQVKKEMILAKFFFIVFTD
ALCWIPIFVVKFLSLLQVEIPGTITSWVVIFILDINSALNPILYTLTTRPFKEMIHRF
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descent (GREAT) |
AF453828
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Bishop,C.E., McElreavey,K. and Agoulnik,A.
Mutations of the GREAT gene cause cryptorc
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/translation="MIVELVFKHLESLRLITMFFLLHFIVLINVKDFALTQGSMITPS
CQRGYEFCGNLTYCLFRAFICDGKDDCGNGADERGCGDTSGWAT FRGTWHGNANSVAL
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TKLKKIFLQHNCIRHISRKAFFGLCNLQILVLNHNCITTLRFGIFKDLHQLTWLILDD
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SVLLLTYLTLEKFLVIVFFFSNIRPGKRQTSVILLCIMMAGFLIAVIFFWNKDYFGNF
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71. .2335
                                                                                                                                                                   /protein_id="AAL73946.1"
/db_xref="GI:18483168"
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                                    TGCTTGGCTAATTTTAGATGACAACCCGATCACCAGAATCTCACAGAAGTCCTTTATGGG
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2539)
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Location/Qualifiers
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GFVPEKFFSSLKNIGELDLSSNNITKLEVHLESDLHLLQKLNISSNPLLYVHKNQFGS
LKQLQSLDLER ELPMISTGME'QPMKNISHYLKTERKÇSYVPHYRTCOMPSTDGISSS
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LFSVGVFDIKYKGQYQKXALLMMESVPCRLLGFLATLSTEVSYLLTFELTELKELVIV
FPSSNLRLGKRQTAVALASIWVTGFLLAAVPFTFREDVFGNFYGKNGVCPFLHYDQAED
EGSRGYSLGIFLGVNLLAFLVIVISYVTMFCSIHKTALQTAEVRSHIGKEVAVANRFF
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/translation="MRILHVILLTEVKDFALADSSMYAPLCPKGYFPCGNLTKCLPR
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NELECVKADLKAVPKVSSNVTLLSLKKNKIHRLPVKVFSRYTELRKIYLQHNCITHIS
RRAFIGGHNLGILXLSHNCITSLRPGIFKDLHQLAWLILDDNFTRISQKSFWGLNSL
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                                                      TGGAGTCTGCTTCCCACTTCATTATGACCAAGCAGAAGATTTTGGAAGTAGAGGGTACTC
                                                                                                                         TCTCATAGCGGCCGTTCCGTTCACCAGAGAGGATTATTTCGGCAACTTTTATGGGAAAAA
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                                                                                                                                                   CGGGAAGGAGGTGGCTTGCAAACCGGTTCTTTTTATCGTGTTCTCTGATGCCATCTG
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                                                                                          ctatactctgaccacaagaccatttaaagaaatgattcatcggttttggtataa
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                                      CTACACTCTGACGACCTCCTTTTTTAAGGACAAGTTGAAACAGTTGCTGCACAA
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AX088165.1
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/protein_id="CAC34686.1"
/protein_id="CAC34686.1"
/protein_id="CAC34686.1"
/db_xref="GI:13397079"
/translation="AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQ
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VKKEMILAKRFFFIVFTDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALN
PILYTLITRPFKEMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRRCHLS"
pilyTLTTTPFKEMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRRCHLS"
pilyTLTTTPFKEMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRRCHLS"
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/db_xref="taxon:9606"
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                                                                    aataagcatgcgcagctgtggatggagagtactcattgtcagcttgtaggatctttggcc 1494
                                                                                                            ttaatgggaatatatttattcgtgatcggaggctttgacctaaagtttcgtggagaatac 1434
                                                                                                                                                  ACGGACGGCATTTCTTCATTTGAGGACCTCTTGGCTAACAATATCCTCAGAATATTTGTC
                                                          CAGAAGTATGCCTTGCTGGATGGAGAGCGTGCAGTGCCGCCTCATGGGGTTCCTGGCC
                                                                                                CTGATGGGTGTTTACTTGTTGTTTGGCATTTTCGATATAAATACCGAGGGCAGTAT 249
                                                                                                                                       ATTAAAGCTGAAAATACAACTCACGCTATGTCCATCAAAATCCTTTGTTGCGCTGATTGC
tgcattgtctatccttttagatgtgtgagacctggaaaatgcagaacaattacagttctg
                               attotgtocacagaagtatcagttttactgttaacatttctgacattggaaaaatacatc
                    ATGCTGTCCACCGAAGTCTCTGTTCTGCTACTGACCTACTTGACTTTGGAGAAGTTCCTG
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Mammalia; Eutheria; Primates; Catarrhini;
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/db_xref="taxon:9606"
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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Michell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Perzy, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Stone, H., Sutson, I., Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Sisson, I., Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Shoshtari, K., Watlinamson, A., Washington, C., Watlinamson, S., Warren, R., Washington, C., Watlinamson, A., Washington, C., Watlinamson, M., Williamson, A., Washington, C., Watlinamson, A., Washington, C., Watlinamson, M., Washington, C., Watlinamson, M., Williamson, A., Watlinamson, A., Washington, C., Watlinamson, A., Watlinamson, A., Watlinamson, A., Washington, C., Watlinamson, A., Washington, C., Watlinamson, A., Washington, C., Watlinamson, A., Washington, C., Watlinamson, A., Watlinamson, A., Washington, C., Watlinamson, A., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329First call findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
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Web site: http://www.hgsc.bcm.tmc.
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
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                                                                                                                                                                                                  CAGAAGTATGCCTTGCTGGATGGAGGGGGGGCGCGCCTCGTGGGGTTCCTGGCC
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                                               ATTTGCATCTGGATGGCGGGATTTTTAATAGCTGTAATTCCATTTTTGGAATAAGGATATT
                                                                                                 GTCATTGTCTTCCCCTTCAGTAACATTCGACCTGGAAAACGGCAGACCTCAGTCATCCTC
                                                                                                                                                ATGCTGTCCACCGAAGTCTCTGTTCTGCTACTGACCTACTTGACTTTGGAGAAGTTCCTG
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Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Sequence 1 from Patent WO0188127
AX356204
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Mammalia; Eutheria;
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/db_xref="taxon:9606".
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Pred. No. 4.1e-40;
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833 atttaactgttttagtgatgaggaaaaacaaaattaatcacttaaatgaaaatacttttg 892

773 tggaccttgaaggcaaccatatccataatttaagaaatttgacttttatttcctgcagta 832

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Query Match 5.4
Best Local Similarity 47.5
Matches 627; Conservative
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G protein-coupled regreat pond snail.
Lymnaea stagnalis
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1 (bases 1 to 3756)
Tensen,C.P., Van Kesteren,E.R., Planta,R.J., Cox,K.J., Burke,J.F.,
van Heerikhuizen,H. and Vreugdenhil,E.
A G protein-coupled receptor with low density lipoprotein-binding
motifs suggests a role for lipoproteins in G-linked signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Mol. Biol., Research, Institute Neurosc Universiteit, De Boelelaan 1083, Amsterdam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-JUN-1993) Cornelis P. Tensen, Dept. of Biochemistry and Mol. Biol., Research, Institute Neurosciences Vrije
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tensen, C.P.
Direct Submission
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TEFKCNNSQCYAFGNLCDGLVDCVDGSDEDQVACDSDKYGCAEGSLIKKEFVCDGWV
DCKLTFADELNCKLCDEDDFRSGDTRCIJKSNVCDGYCDCKTCDDEEVQANUTYGCPM
DTKYMCRSIYGEPRCIDKDNVCNMINDCRDGNVGTDEYYCSNDSECKNFQAAMGFFYC
PEERCLAKHLYCDLHPDCINGEDEQSCLAPRCSQDEFQCHHGKCIPISKRCDSVHDC
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FRCKNQCIDFLQVCVKGDKYDGCADQSHLINCSQHICLEGQFRCRKSFCINQTKVCD
GTVDCLQGMMDENNCRYWCPHQOAICQCEGVTMDCTGQKLEMFVQOMEEDLSKLMIG
DNLLNLTSTTFSATYYDKVTYLDLSRNHLTEIPIYSFQNMWKLTHLNADNNITSLKN
GSLLGLSNLKQDHINGRKIETLEDDTFSSMIHLTVLDLSRQRLTHYVKNMFKGLKQIT
VLN1SRNQLKGPKQDEFSSCEDLMSNHVLTEIPIYSFQNMWKLTHLNADNRTDERRGK
VHSFLLTNLAIGDFLMGVYLLIATADTYYRGYVISHDENWKQSGLCQFAGFVSTFSS
ELSYLTLSTTLAIGDFLMGVYLLTIATADTYYRGYVISHDENWKQSGLCQFAGFVSTFSS
ELSYLTLSTTLDRLICILFPLRKTRLGLRQAIIVMSGUMVLVFLLKAULGFEXFE
ELSYLTLSTTELDRLICILFPLRKTRLGLRQAIIVMSGUMVLVFLLAVLPLLGFSYFE
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/product="G protein-coupled receptor"
/protein_id="CAA80651.1"
/db_xref="GI:438129"
/db_xref="SWISS-PROT:P46023"
/db_xref="SWISS-PROT:P46023"
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/db_xref="taxon:6523"
/tissue_type="Central nervous
/dev_stage="Adult"
วาล - >==="
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851 c 890 g 987 t
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RTAESKNDNAMARRWTLIVMTDFCCWVPIIVLGFVSLAGARADDQVYAWIAVFVLPLN
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HCDDGMLQCvLmgSKCDGVSDCENGMDESVETCGCLQSEFQCNHTTC1DK1LRCDRND
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                        5.48;
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Pred. No. 1.5e-29;
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                                                                                                         TCGTGCTCATAGCCTCCTCTTACCTTTGGATGTTTCAGTAGCCAAAAAAGACCCGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-432E15 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Nov 10, 2000 this sequence version replaced gi:11121365. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL138708

AL138708

Human DNA sequence from clone RP11-432E15 on ch
STSs, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 http://www.sanger.ac.uk/HGP/Chr13 This sequence is the entire insert of clone RP11-432E15 The true left end of clone RP11-154I23 is at 137612 in this sequence. The true right end of clone RP11-95M14 is at 13246 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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1. (bases 1 to 170522)
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1456. .1750
/note="Alusx repeat: matches 3.
2078. .2183
                                                                                                                                               208. .299
                                                                                                                                                                                                                     194.
                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11.2"
19. .289
                                                                                                       /note="23 copies 4 mer tgtg 77% conserved"
                                                                                                                                                                                 /note="53
                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-432E15"
                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                            .300 of consensus"
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13 Contains
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12713. 12980

/note="sequence from overlapping cl
(AL136106) Assembly confirmed by re
13272. 13417

/note="MIR repeat: matches 38. .188

complement(13670. .13919)

/note="match: GSS: Em:AQ021664"

complement(13740. .14130)

/note="match: GSS: Em:AQ032630"

13771. 14227
                                                                                                                                                                                                              complement(17019. .17275)
/note="match: GSS: Em:AQ452676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11234. .11331
/note="sequence from overlapping (ALI36106) Assembly confirmed by complement(11953. .12400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9078. .9121
/note="11 copies 4 mer caca 100%
complement(9603. .10104)
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/note="sequence from overlapping (AL136106). Assembly confirmed by
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2600..3122
2600..3122
/note="match: GSS: Em:AQ529216"
2646..2940
/note="AluSg repeat: matches 1..302 of consensus
3590..3894
                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1. .312 of consensus" 16656. .1680
                                                                                                                                                                                                                                                                                                                                                                                      /note="MER1B repeat:
16343. .16655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="50 copies 2 mer at 63% conserved"
7396. .7487
/note="23 copies 4 mer atat 66% conserved"
7884. .7915
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/note="L2 repeat: matches 2575. .2694 of consensus
5788. .6085
/note="AluJo repeat: matches 3. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSq repeat: matches 1. 3926. .4462 // 3926. // 3926. // 462 // 468. .4805 // 4688. .4805 // 4688. .4805 // 4688. // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4805 // 4
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Note="sequence from overlapping clone object of the object 
                                                                                                                                                                                                                                              /note="MER1B repeat: matches 244.
complement(17019. .17275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="sequence from overlapping (AL136106).Assembly confirmed by
                                                                                                                                              'note="match: GSS: Em:AQ511484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 15. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match: GSS: Em:AQ569313"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluJb repeat: matches 1. .302 of consensus"
220. .8376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER20 repeat: matches 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 2515. .2750 of consensus"
       GSS: Em:AQ358157"
                                                                          GSS: Em:AQ817416"
                                                                                                                                                                                                                                                                                                                                                                                                                      matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      .244 of
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restriction digest."
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restriction digest."
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                                                                                                                                                                                                                                                                                  .305 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by restriction
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   δÃ
                                                                       Query Match
Best Local Similarity
Matches 278; Conserv
misc_feature
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/note="L2 repeat.
28639. .28960
/note="AluSq repeat: matches 1...
/no489. .29861
/no489. .29861
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/note="L2 repeat: matches 2006.

/complement(29720. .30187)

/note="match: GSS: Em:AQ317477"
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/note="12 repeat: matches 2617.

25636. .25785
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/note="L2 repeat: matches 2381. .2617 of consensus" 23961. .24213
/note="Alusx repeat: matches 47. .299 of consensus"
                                                                                                                                                                                                              /note="AluSx repeat: matches 1.
40873. .41144
/note="AluY repeat: matches 39.
                                                                                                                                                                                                                                                                                                                                                                                      39703. .39750
/note="24 copies 2 mer ca 75% conserved"
39859. .39976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 96. .148
36429. .36961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(36043. .36433)
/note="match: GSS: Em:AQ816559"
36420. .36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32462. .32774
/note="AluSx_repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER5A repeat: matches 1.
complement(30119. .30414)
note="match: GSS: Em:AQ230143"
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21080. 21392
/note="Aluyb repeat: matches 1.
21395. 21538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ284653
match: STS: Em:G55301"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L2 repeat: matches 2248.
complement(35852. .36413)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39203. 39242
/note="20 copies 2 mer ca 100% conserved"
39250. 39648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="12 repeat: matches 2307. .2710 of
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                                                                                                       5.2%;
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                                                                                                                                                                                                              repeat: matches 39.
                                                                       Score 187.4; DB 9;
Pred. No. 2.9e-28;
0; Mismatches 151;
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                                                                                                                                                                                                                                                                                  .296 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .310 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L0875; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 164180 bases at least Q40
Consensus quality: 168742 bases at least Q30
Consensus quality: 171594 bases at least Q20
Consensus quality: 171594 bases at least Q20
Insert size: 174665; sum-of-contigs
Insert size: 185918; 5.0% error; agarose-fp
Quality coverage: 3.37x in Q20 bases; sum-of-conti
* NOTE: This is a 'working draft' sequence. It of consists of 20 contigs. The true order of the * is not known and their order in this sequence
                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk On Aug 27, 2000 this sequence version replaced gi:9863462.
                                                                                                                                                                                                                                          Center project name: bA15909
----- Summary Statistics
                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                              Center: Sanger Centre
Center code: SC
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AL136106.4 GI:9931223
HTG; HTGS_PHASE1; HTGS
                                                                    coverage: 3.36x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 176565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 13 clone RP11-15909, *** SEQUENCING PROCRESS ***, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                    sum-of-contigs Quality
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161962 164531
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54903. .65169
/note="assembly_fragment:00809
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/db_xref="taxon:9606"
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31314: contig of
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54802: contig of 2746 bp in length

54902: gap of 100 bp

65269: gap of 10267 bp in length

65269: gap of 100 bp

7508: contig of 10239 bp in length

7568: gap of 100 bp

80749: contig of 5141 bp in length
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44166: contig of 11
1266: gap of 10
51956: contig of 7
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169371: contig of 4740
9471: gap of 100 k
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120411: contig of 11616 b
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37: gap of 100 bp
16458: contig of 10671 bp in length
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contig of 2570 bp
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contig of 20264 b
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contig of 7122 bp
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                                                                                                                        TAATTCCATTTTGGAATAAGGATTATTTTGGAAACTTTTATGGGAAAAATGGAGTATGTT
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                          ttcttggta 1777
                                                                                                                                               tcattccattgagcaataaggaatttttcaaaaaactactatggcaccaatggagtatgct 1708
                                                                                                                                                                                        GAAAACGGCAGACCTCAGTCATCCTCATTTGCATCTGGATGGCGGGATTTTTAATAGCTG
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                                                                                       tccctcttcattcagaagatacagaaagtattggagcccagatttattcagtggcaattt 1768
                                                                                                                                                                                                                                                     CCTACTTGACTTTGGAGAAGTTCCTGGTCATTGTCTTCCCCCTTCAGTAACATTCGACCTG
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                                                           TCCCACTTTATTATGACCAAACAGAAGATATTGGAAGCAAAGGGTATTCTCTTGGAATTT 98184
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Pred. No. 2.9e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RS. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Choma, T., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, R., Choma, T., Christopoulos, C., Cleveland, T., Davis, C., Chen, R., Chen, G., Chen, R., Chen,
                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Direct Submission

Submitted (26-OCT-2001) Human Genome Sequencing Center, Departor Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:17064612.
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Rattus norvegicus clone CH230-148B15, *** SEQUENCING
***, 66 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                        findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                   Center project name: GILC Center clone name: CH230-148B15
                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
                                                                  Assembly program: Phrap; version 0.990329First call
quality: 139190 bases at least Q40
                                                                                                                                                                                                             Project Information
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 124603 bases at least Q30
Consensus quality: 124715 bases at least Q30
Consensus quality: 124807 bases at least Q20
Insert size: 135122; sum-of-contigs
Quality coverage: 13.31 in Q20 bases; sum-of-contigs
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Submitted (24-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jan 26, 2002 this sequence version replaced gi:18308770.
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AC108017.2 GI:18376924
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/clone="CTD-2005A22"
                                                                                                     ocation/Qualifiers
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Homo sapiens BAC clone RP11-719M18
AC019341 GI:15341625
                                                               Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Aug 29, 2001 this sequence version replaced gi:14091943.
                                                                                                                                                                                                       Submitted (29-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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Submitted (01-JAN-2000) Genome
University School of Medicine,
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Radionenko, M., Cordum, H. and Hawkins, M.
The sequence of Homo sapiens BAC clone RP11-719M18
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                   Waterston, R.
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Waterston, R.H.
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19064. .63219
/note="assembly_name:Contig42"
ture 6320. .125322
/note="assembly_name:Contig43"
38309 a 23846 c 23694 g 39273 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Location/Qualifiers
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NEIGHBORING SEQUENCE INFORMATION:
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972. .1001
                                                          /rpt_family="MalR" 6353. .6733
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/clone_lib="RPCI-11"
505. .553
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/db_xref="taxon:9606"
/chromosome="4"
  rpt_family="MER1_type"
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                                                                                                                                                                                                                                _family="ERV1"
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26508
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24855
                                      /rpt_family="CT-rich"
28322. .28626
                                                                                                                                                      /rpt_family="(TA)n"
27781. .28057
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27761. .27781
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12071. .12388
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16105. .16445
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30-SEP-1999. WO9948921-A1 Homo sapiens

WPI; 1999-591074/50. P-PSDB; AAY42171.

Hsueh AJW, Hsu SY,

Liang Ś

Van

Der Spek

New G-protein coupled receptors, useful for identifying their own

(STRD) UNIV LELAND STANFORD JUNIOR. (ORGA) ORGANON NV.

25-MAR-1999;

26-MAR-1998;

98US-0079501. 99WO-US06573.

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Human G protein coupled prevention, diagnosis an and immune diecase.
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The invention provides human G protein coupled protein receptor (HGPRP) polypeptides and polynucleotides encoding them. The polypeptides can be produced by standard recombinant methodology. The polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression. Diseases that can be treated are cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis and hepatitis), cancers (e.g. leukemia, melanomas and adenocarcinoma), immune disorders (e.g. anemia, asthma and Crohn's disease) and neurological disorders (e.g. epilepsy, Alzheimer's disease and Parkinson's disease). The anti-hGPCR antibodies may also be used as diagnostic agents for detecting the presence of HGPRP polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). Sequences AA290521-526 represent cDNA fragments encoding the HGPRP polypeptides

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03-DEC-1999;
12-JAN-2000;
                                                                                                                                          Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G protein-coupled receptor; GPCR; CON222 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychiatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease depression; migraine; genetic screening; ds.
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Claim 22; Page 15-16; 215pp; English.

The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein-coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating schizophrenia. These compounds are also useful for treating schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder, epilepsy, neuritis, neurasthenia, neuropathy, neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are uigraine and senile
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  2000US-0179065.
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2000US-0184664.
2000US-0198074.
2000US-0199123.
2000US-029467.
2000US-0216486.
2000US-0216647.
2000US-0216647.
2000US-0217496.
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2000US-0217496.
2000US-0218299.
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2000US-0218299.
2000US-0225964.
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08-DEC-2000
                                                                   The nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                               Isolated digestive system associated polypeptide for treating, preventing and/ or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection e.g. diagnosis -
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P-PSDB; AAM99945.
                            Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                         The invention relates to novel genes (AAI99548-AAI99604) and proteins (AAM9936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                     Claim
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2000US-0234274. 2000US-0234997. 2000US-0234998. 2000US-0235484. 2000US-0235834.

2000US-0236368. 2000US-0236369. 2000US-0236370. 2000US-0236370. 2000US-0237037. 2000US-0237038.

2000US-0237039.
2000US-0237040.
2000US-0239935.
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2000US-024960.
2000US-0241221.
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Listing;

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2000US-0241786 2000US-0241787

2000US-0229344 2000US-0229509 2000US-0229509 2000US-0229513 2000US-0231242 2000US-0231242 2000US-0231243 2000US-0231243 2000US-0231241 2000US-0231414 2000US-0232080 2000US-0232080 2000US-0232080 2000US-0232080 2000US-0232080 2000US-0232080 2000US-0232398 2000US-0232399 2000US-0232401 2000US-0233401 2000US-0233063 2000US-0233063 2000US-0233063

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cardiant; gene therapy; cancer; immune disorder; cardiova:
neurological disease; infection; human; secreted protein;
musculoskeletal system; ss.
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  2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0184664.
2000US-019874.
2000US-019974.
2000US-019974.
2000US-0199467.
2000US-016647.
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Note: The sequence da
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s related to the musculoskeletal system including
keletal cancers and also for testing and detection e.g.
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2000US-0250130.

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2000US-0251869.

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                                        99WO-US24206
                                                                                                                                                                                                                                                                                                                      depression; psoriasis;
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CC sequence tags (sESTS), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoletic; chemotactic; antibacterial; antifungal; antiviral; antifinflammatory; cc chemokinetic; antiparkinsonian; antipsoriatic; cerebroprotective; cc antiasthmatic; vulnerary; antifucer; osteopathic; neuroprotective; cc nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; cc anticonvulsant; and antidepressant. The sESTs can be used for gene criterapy and in vaccines. The sESTs are useful as probes for the correspond to the sESTs. Proteins encoded by the sESTs care useful in assays for determining biological activity and raising care useful in assays for determining biological activity and raising care useful in assays for determining biological activity and raising contibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions costeoparthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation cdisorders (haemophilla, thrombosis), inflammatory disorders (Crohn's Cdisease), tumours, bacterial, fungal or viral infections, depression and corriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA43426
sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides, and encoded proteins, comprising secreted d sequence tags (sESTs), useful for treating various disorders autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to AAA45925 represent specifically claimed secreted expressed tags (sESTs), isolated from human, mouse, chicken and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 593; 803pp; English.
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Treacy M,
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           aaaattaatttataataatagctaagataaatattttacaaggacatgaggaaaaataaa 2434
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                                                                 cgcagagaatactgtgggggtgcttcatgagggatttactggtatgaaaatgaataccac
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                                                   cgcagagaatactgtgggggtgcttcatgagggatttactggtatg
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98.7%;
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0; Mismatches
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2000US-0246528
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Best Local Similarity

99.8%;

1.1e-113; hes 0;

Indels

0;

Gaps

0

61 1803

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CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are consisted from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC Note: The senuence data for this
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
07-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                       Isolated digestive system associated polypeptide for treating, preventing and/or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection
                         Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                           Claim 1;
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DB; AAM99972.
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Query Match

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                                                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
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neurological disease; infection;
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                                                                                                                                                                                                                                               musculoskeletal system related
 2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-018350.
2000US-018974.
2000US-0190874.
2000US-0190875.
2000US-0199123.
2000US-0205515.
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                                                                                           2001WO-US01338
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                           system;
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1; Mismatches
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481

2163

361

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301 2043 1983 181

241

immune disorder;

protein;

cardiovascular disorder;

antiulcer;

polynucleotide

SEQ

IJ NO

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20-OCT-2000;
20-NOV-2000;
21-NOV-2000;
21-NO
                                                                      Claim
                                                                                                     Isolated polypeptide for disorders related to the musculoskeletal cancers \epsilon diagnosis .
                                                                                                                                                                                         WPI; 2001-451937/48.
P-PSDB; ABB04062.
                                                                                                                                                                                                                                              Rosen
The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by
                                                                       1;
                                                                                                                                                                                                                                            CA,
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                                                                                                                     r treating, preventing and/or prognosing musculoskeletal system including and also for testing and detection e.g.
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parasitic infections.
Note: The sequence da
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Human; gene therapy; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
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                                                            Human cDNA SEQ ID NO: 137.
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proliferative disorder; inflammation; ss.
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                                     standard;
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Matches 528
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Note: The sequence data for this patent did not form part of the pr specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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DB; AAU18108.
tcattcatctgggtggaaatgtggccactgcaggagatgccacctgagttaatgaagccg
                                                                                                              tggtataactacagacaaagaaaatctatggacagcawaggtcagaaaacatatgctcca
                                                                                                                           tggtataactacagacaaagaaaatctatggacagcaaaggtcagaaaacatatgctcca
                                                                                                                                                                       ttgaacccaattctctatactctgaccacaagaccatttaaagaaatgattcatcggttt
                                                                                                                                                                                                                                 gaaataccaggtaccataacctcttgggtagtgatttttattctgcccattaacagtgct
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99.8%;
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2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-0225270.

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ARSSULT 12
ARS2957
XX ARS295
XX Endocr
KW Cat; d
KW Cat; d
KW Cat; d
KW Cat; d
KW Wound
KW Hungal
KW Hungal
KW Wound
KW WOOOOL
KW TISSUE
XX ARS295
XX ARS29
11-JUL-2000;

11-JUL-2000;

11-JUL-2000;

126-JUL-2000;

26-JUL-2000;

14-AUG-2000;

15-AUG-2000;

16-AUG-2000;

17-AUG-2000;

18-AUG-2000;

19-AUG-2000;

23-AUG-2000;

24-AUG-2000;

25-AUG-2000;

26-AUG-2000;

27-AUG-2000;

28-AUG-2000;

29-AUG-2000;

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21-SEP-2000;

21-SEP-2000;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular fundamental process such as cardiac arrest.
                                                                                                                                                                                                                                                                      Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sumburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                        1744
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P-PSDB; AAU18344.
                                 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/or prognosing disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnosis
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gcccagatttattcagtggcaattttcttggtattaatttggccgcatttatcatcata
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2000US-0249297

2000US-0249299

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2000US-025198

2000US-025198

2000US-0251866

2000US-0251866

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Pred. No. 1.1e-113;
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2000US-0232391
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2000US-0246231

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia; blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; neoplastic disorder; nephtoma; autolmmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder; ss.
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2000US-0186628.
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2000US-0198174.
2000US-0198123.
2000US-020515.
2000US-0209467.
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CC disorders (e.g. anaemia or blood coagulation disorders), ce lettrolyte imbalance disorders (e.g. hypertania), co repolastic disorders (e.g. hypertania), co disorders (e.g. hypertania), co disorders (e.g. renal failure or mephritis), co disorders (e.g. renal failure or mephritis), co disorders (e.g. nemal failure or myocardial infarction), co blood disorders (e.g. anaemia or blood coagulation disorders), co neoplastic disorders (e.g. nephromatoramia) or hypertania), co neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune co diseases, cancers, inflammatory diseases, reproductive system co disorders, wound healing and respiratory disorders. AAS30165-AAS30251 co acid sequences of the invention. Note: The sequence data for this cardial sequences of the invention. Note: The sequence data for this cardial sequences of the invention.
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Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid

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cc for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human cc tissues disclosed in the specification. The nucleic acids, proteins, cc antibodies and (ant)agonists are useful in the diagnosis, treatment can prevention of: (a) cancer, e.g. breast and ovarian cancer and co other cancers of the adrenal gland, bone, bone marrow, breast, cc gastrointestinal tract, liver, lung, or urogenital; (b) immune cd disorders e.g. Addison's disease, allergies, autoimmune haemolytic multiple scierosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and cc parasitic infectious diseases such as viral, bacterial, fungal and
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Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel (ABB03087-ABB04109) associated
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б -	Db 143 TTTTCAGATAGTTTCAAATACACCAAAAATGTTTGAAACACAAAAATACTGGAATCAAAC 84
IC 3534	Qy 3475 ttttcagatagtttcaaatacnccaaaaatgtttgcaacacaaaaatactggaatcnaac
ด์ -	Db 203 CTACGTTATTAGAATTTTTTGCTTTCATAATGTGAAACCTTTAAGCAGGAGAAGAAAATG 144
.g 3474	Qy 3415 ctacgttattagnattttttgctttcataatgtgaaacctttaagcaggagaagaaaatg
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PRIOR APPLICATION DATA: APPLICATION UNMBER: US 08 FILLING DATE: 27-0CT-1997 APPLICATION NUMBER: PCT/G FILLING DATE: 01-APR-1996 APPLICATION NUMBER: GB 95 APPLICATION NUMBER: GB 95 APPLICATION NUMBER: 32.9 FILLING DATE: 31-MAR-1995 ATTORNEY/AGENT INFORMATION: NAME: MS MATY J Wilson REGISTRATION NUMBER: 32.9 REFERENCE/DOCKET NUMBER: 32	1 -585-4 -6287 NO. 6287 APPLICAN APPLICAN APPLICAN APPLICAN CORRESPO ADD STH CIT STH CIT STH COUNTES MEI COMPUTES MEI COMP	44 4444 44 444 444 444 444 444 444 444
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APPLICATION NUMBER: US FILLING DATE: 27-OCT-199 APPLICATION NUMBER: US FILLING DATE: 01-APR-199 APPLICATION NUMBER: GB FILLING DATE: 01-APR-199 APPLICATION NUMBER: GB FILLING DATE: 31-MAR-199 RNEY/AGENT INFORMATION: NAME: MS MAT'I ON NUMBER: STANDICATION NUMBER: AS MAT'I OF TELEPHONE: (703) 816-4100 NUMBER: 816-4100 NUMBER: 816-4100 NUMBER: 878ANES (703) 816-4100 NUMBER: 878ANES (703) 816-4100 NUMBER: 878ANES (703) 816-4100 NUMBER: 878ANES (878ANES) STANDINGERS: COMBUNICATION: 816-4100 NUMBER: 878ANES (878ANES) STANDINGERS: COMBUNICATION: 878ANES (878ANES) STANDINGERS: COMBUNICATION: 10-64 TYPE: NUCLEIC COMBUNICATION: 10-64 TYPE: CDNATHETICAL: NO	TEN TOUCH	4203 4203 2317 3974 2296 615 1912 4758 4758 4758 4758 4758 1677 51677 51677 51677 51677 51677
1/68 DATA: NUMBER: 27-0CT: NUMBER: 01-APR: 01-APR: 11-APR: NUMBER: 11-MINIMBER: 11-MINIMBER: NUMBER: N	S/093535 Mark S David A Jonathan Plant Thereo RESS RESS RESS RESS RES RES RES RES RES	040400400440H
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GENERAL INFORMATION:
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Best Local Similarity
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ORIGINAL SOURCE:
ORGANISM: TO
STRAIN: Cf2
                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 8th Floor, 1100 No. 6
COMPUTER READABLE MEDIUM TYPE:
                                                                                                                                                                                      APPLICANT: Dixon, Mark S
Jones, David Jones, Jonatha
                                                                                                                                                                         TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                             AACTTGTCTAGGTTGAATCTTGTTAATAATCAGCTTTCTGGCTCTATTCCTGCTTCATTG 105
                           CITY: Arlington
STATE: Virginia
COUNTRY: United States
ZIP: 22201-4714
                                                                                                                                                                                                                                                                   Application US/09353585
                                                                                                                                                                       Jones, Jonathan DG INVENTION: Plant pathogen resistance
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45.1%;
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS Mary J Wilson
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
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LENGTH: 6471 base pairs
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ggcaaccatatccataatttaagaaatttgacttttatttcctgcagtaatttaactgtt
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                                                            GGCT----CTATTCCTGCTTCATTGGGGGAATTTGAACAACTTGTCTTTTTTGTTTAT
                                                                                               cgtttacctgataaacctctctgtcaacacatgccaagactacattggctggaccttgaa
                                                                                                                                         ccaacattttatggactaaattctctttattctcttagtcctgatgaataacgtcctcacc 723
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide LOCATION: 1677..1753
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Pred. No. 2.7e-05;
0; Mismatches 317; Indels
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SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 2687731
US-09-131-648-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.6%;
Best Local Similarity 47.5%;
Matches 174; Conservative
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APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACELULIAR ADHESIVE
FILE REFERENCE: PF-0576 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-08-10 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/131,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2742 GGGAATCTGAACAACTTGTCTATGTTGTATCTTTACAATAACC 2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2562 GGAAATCAGCTTTCTGGCTCTATTCCTGAAGAATAGGTTACCTAAGATCTCTTAATGTC
  869
                                                                                                                                                                                                                                                                                                                                                                                                                                819 tatttcctgcagtaatttaactgttttagtgatgaggaaaaacaaaattaatcacttaaa 878
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caatct 703
                                                                                                                                                                                                                                                                                                                                               tgaaaatacttttgcacctctccagaaactggatgaattggatttaggaagtaataagat 938
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                                      gaatct 1124
                                                                                                                                                                                                                                                                                                                                                                                                        aaaccttactggcctggatttatctcaaaacaatttatcttcagtcaccaatattaatgt 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTTGTCTAGGTTGAATCTTGTTAATAATCAGCTTTCTGGCTCTATTCCTGCTTCATTG 2741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttagtgatgaggaaaaacaaaattaatcacttaaatgaaaatacttttgcacctctccag 903
                                                                                                      tctcagcctagaagggattgaaatttcaaatatccaacaaggatgtttagacctcttat 1118
                                                                                                                                                                                                  ctataatccaatccagaaaattcaagcaaaccaatttgattatcttgtcaaactcaagtc 1058
                                                                                                                                                                                                                                                                             tgaaaatcttccaccgcttatattcaaggacctgaaggagctgtcacaattgaatctttc 998
                                                                                 tctgatgattggggaaaatccaattatcagaatcaaagacatgaactttaagcctcttat
                                                                                                                                                                                                                                          ttctacaatttcacctggagcctttattggcctacataatcttcttcgacttcatctcaa 577
                                                                                                                                                                                                                                                                                                                         tgaaaaatgtctgtccgaactgagcaacttacaagaactctatattaatcacaacttgct
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Pred. No. 3.2e-05;
0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2290;
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US-07-741-453A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-741-453A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4417 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/
FILING DATE: 19911015
CLASSLETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9
1554
                                    1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  1254 TGTACTCCTAAGTCAGATGAGTTCAACCCCTGTGAAGACATAATGGGCTACAAGTTCCTG 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1615 L STREET, N.W. CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
GGTTTCTTCACTGTCTTTGCCAGTGAATTATCAGTGTATACACTGACAGTCATCACCCTG
                          ggatctttggccattctgtccacagaagtatcagttttactgttaacatttctgacattg 1542
                                                                                              cgtggagaatacaataagcatgcgcagctgtggatggagagtactcattgtcagcttgta 1482
                                                                                                                                                                                                                              GTCCTCCTTACCAGTCACTACAAATTGACTGTCCCACGCTTTCTCATGTGCAACTTGGCC
                                                                                                                                                                                                                                                        atgcgaccttatatcaggtctgagaacaagctgtatgccatgtcaatcatttctctctgc 1362
                                                                                                                                                                                                                                                                                                                              agagtatttgtctgggttgtatctgcagttacctgctttggaaaacatttttgtcatttgc 1302
                                                                          CATTCTGAGTACTACAACCATGCCATCGACTGGCAGACAGGCCCTGGGTGTAACACAGCT
                                                                                                                                                                                      tgtgccgactgcttaatgggaatatatttattcgtgatcggaggctttgacctaaagttt 1422
                                                                                                                                                                                                                                                                                                        AGGATTGTGGTGTGTTAGTCTGCTGGCTCTCCTGGGCAATGTCTTTGTCCTGATC 1373
                                                                                                                                                    TTTGCAGATTTCTGCATGGGGATGTATCTGCTCCTCATCGCCTCCGTAGACCTCTACACT
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LIBERT, FREDERIC
DUMONT, JACQUES
VASSART, GILBERT
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/741,453A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.8; DB 4
Pred. No. 0.0004;
0; Mismatches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            192;
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                                                                                                                                                                                                             Query Match 1.4%;
Best Local Similarity 48.0%;
Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J Timothy
REGISTRATION NUMBER: 38,2
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
2394 agctaagataaatattttacaaggacatgaggaaaaataaaaatgactaatgctcttaca 2453
                                                                                          2274 actcaattcctattcatgactgactctgaaattcatttcttcgcagagaatactgtgggg 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                            529 AATGAATATAATTAATAAATAATAAAAAATTAATAATAAGAAATTAAAGTTAAAATTA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                     1137, Application US/08998416
5. 6239264
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[: 3054 Cornwallis Road

Research Triangle Park

: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             636 base pairs
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Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                 PAG1692RP
                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                             Score 50.8; DB 4;
Pred. No. 0.0018;
0; Mismatches 157;
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; NAME/KEY:
; LOCATION:
US-08-487-886-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: (617) 723-8923 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2454 aagggaagtaattatatcaataatgtatatatattagtagacattttgcataagaaatta 2513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vul Yen
APPLICANT: Nugent, No. 5744448een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
                                                CLONE: pHFSHR11-11, pHFSHR15-6
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1BM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,886
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" di
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                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: US
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 ATTTTAATAATAATTCTTATAAAAAGATTAAATAATATATAAATCAACATAATATTTATAAA 410
                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Boston
                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/6 FILING DATE: 15-MAR-1991
                                                                                                                          ORGANISM: HOTISSUE TYPE:
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                       ENGTH:
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                  protein coding region 75 to 2159
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Best Local Similarity
                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                     CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
NAME: Gass, David B.
NAME: Jay 153
                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,070A
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SECULARY OF SECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: de la Chapelle, Albert
APPLICANT: Aittomaki, Kristiina
APPLICANT: Huhtaniemi, Ilpo
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                                                                                                                         REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196
                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illino
                                         LENGTH:
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             STRANDEDNESS:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
linear
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US-08-482-855-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6;
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1389 tttattcgtgatcggaggctttgacctaaagtttcgtggagaatacaataagcatgcgca 1448
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                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                     NAME: Williams, Stephan P. REGISTRATION NUMBER: 28546
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
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US/252
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Pred. No. 0.0033;
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US-08-482-855-1
                                                                                                                                                                                                                                                                          Sequence 28
Patent No.
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Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                  APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1376
                                                                                                                                                                                                                                                                                                                                                                                              1436 GCTGTCAGTCTACACTCTGACAGCTATCACCTTGGAAAGAT 1476
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic acid
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                      ADDRESSEE:
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                                                                                                                                                                                                                                                                            288, Application US/08998416
5. 6239264
3054 Cornwallis
                                                                                                                                                                            Mohr, Christine
                                                                                                                                                                                             Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                     Philippsen, Peter
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                  No.
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                  6239264artis Corporation
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RESULT 10
US-07-757-342D-9
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                                                                                                                                                                                                    Sequence 9, Application US/07757342D Patent No. 6218509
GENERAL INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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hes 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                          NAKAMURA, KAZULO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID G. CONLIN; DIKE, BRONSTEIN,
                                                                                                                                                                                       APPLICANT: IGARASHI, Masao
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No. 6239264th Carolina
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               CITY: Boston
STATE: Massachusetts
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COUNTRY: US
                                                   STREET: 130 Water Street
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N: 435
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Pred. No. 0.0045;
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ZIP: 02109 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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Best Local Similarity 44.8%;
Matches 182; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
CLASSIFICATION: <Unknown>
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LOCATION:
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STRANDEDNESS: double
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                                        Takashi
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Best Local Similarity 44.8%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                1407
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                          1527 aacatttctgacattggaaaaatacatctgcattgtctatcctttt 1572
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1371 CACCGTCATCACTCTAGAAAGATGGCACACCATCACCTATGCTATT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF CUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID G. CONLIN; DIKE, BRONSTEIN CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                              CATGACTGTTCTTTTGTTCTCCTGACAAGTCGTTACAAACTTACAGTGCCTCGTTTTCT 1190
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                                                                                                          tcattgtcagcttgtaggatctttggccattctgtccacagaagtatcagttttactgtt 1526
                                                                                                                                                                      AGTTGATTCCCAAAACCAAGGGCCAGTACTATAACCATGCCATAGACTGGCAGACAGGGAG
                                                                                                                                                                                                                                                       CATGTGCAATCTCCTTTGCAGACTTTTGCATGGGGCTCTATCTGCTCCTCATAGCCTC 1250
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2987 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 130 Water Street
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GENERAL INFORMATION:

APPLICANT: Dixon, Mark S
APPLICANT: Jones, Mark S
APPLICANT: Jones, David A

APPLICANT: Jones, David A

APPLICANT: Jones, Jonathan DG

TITLE OF INVENTION: Plant pathogen resistance genes and
FILE REFERENCE: 620 - 53

CURRENT APPLICATION NUMBER: US/09/180,439

CURRENT FILING DATE: 1998-12-06

EARLIER APPLICATION NUMBER: PCT/GB97/01249

EARLIER FILING DATE: 1997-05-08
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; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-180-439-1
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APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kosta
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
APPLICANT: Jones, Jonathan DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09180439 Patent No. 6225532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09180439 Patent No. 6225532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
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EARLIER FILING DATE: 1996-09-24
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof FILE REFERENCE: 620 - 53
                                             EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
                           EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1898
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APPLICATION NUMBER: GB 9619924.5 FILING DATE: 1996-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2055
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-180-439-2
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CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER FILING DATE: 1996-09-24
NUMBER: OF SEQ. ID NOS: 10
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                                                                                                                                                                                                                                                         ; LENGTH: 4123
; TYPE: DNA
; ORGANIZM: Lycopersicon esculentum
US-09-180-439-7
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US-09-180-439-7
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Best Local S
Matches 134
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                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 7
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APPLICANT: Dixon, Mark S
                                                                                                                                                         Query Match
Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
FILE REFERENCE: 620 - 53
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
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                    504 tacatccatctccatctatgctttcagaggactgaatagccttactaaactgtatctcag 563
                                                                                                  444 tcctgattgcttcaagaattatcatgatcttcagaagctggacctgcaaaacaataagat 503
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ttctggctctattcctgaagaaataggttacctgagttctcttactgaactatatttggg
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milarity 48.2%;
Conservative
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Pred. No. 0.023;
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                                                                                                                                                                                                DB 4;
                                                                                                                                                             144;
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                                                                                                                                                           Indels
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US-08-232-463-14/c
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
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                                                                                                                                                                                             ; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                      Query Match 1.3%; Score 47; DB 1; Length 7218; Best Local Similarity 4.2%; Pred. No. 0.041; Matches 14; Conservative 186; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703)683-4109
TELEZEY: ADDITION:
TELEPHONE: (703)683-4109
TELEPHONE: (703)633-4109
                                      1459
                                                                2964 ttaaatgaacatcatcatatggaattggaataggaggtatgagtacggcagagaagtgg 3023
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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STATE: VA
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                                       Hsueh AJW, Hsu SY,
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                                                                                                                  Homo sapiens.
     Ligands
          New G-protein coupled receptors, useful for identifying their own
                                                   (STRD ) UNIV LELAND STANFORD JUNIOR.
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Human; LGR4; LGR5; LGR7; G-protein coupled receptor; gene therapy; extracellular leucine rich repeat region; mapping; identification.

Human LGR7 short form protein sequence

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Pred. No. 0;
2; Mismatches
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identification.
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                                                                                                                                                                                                                                                                                                                                                                                  Human; G protein-coupled receptor; GPCR; CON222 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychiatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease depression; migraine; genetic screening.
                                               Domain
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE02498
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                                                                                                                                            /label= ir......
66..78
/label= Intracellular_domain
/note= "First IC loop"
                                          /label= Extrace
/note= "First I
125..156
                                                                                                               /label-
104..124
/label=
157..166
                                                                                                                                                                                                                                                                         Location/Qualifiers 42..65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                  - Transmembrane_domain_(1TM)
                                                             Extracellular_domain First EC loop"
                     Transmembrane_domain_(3TM)
                                                                                                                                    Transmembrane_domain_(2TM)
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
03-DEC-1999;
12-JAN-2000;
                     their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder, attention deficit disorder, epilepsy, neuritis, neurostathenia, neuropathy, neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present sequence is human CON222 G protein-coupled receptor (GPCR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1999;
27-OCT-1999;
27-OCT-1999;
27-OCT-1999;
                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                     Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia as well as for identifying compounds useful for treating schizophrenia
                                                                                                                                                                                                                                                                                                                              WPI; 2001-328653/34.
N-PSDB; AAD06507.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doma in
                                                                                                                                                                                                                                 Claim 1; Page 15-16;
                                                                                                                                                                                                                                                                                                                                                                                              (PHAA)
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                                                                                                                                                                                                      invention relates to human G protein-coupled receptor (GPCR) and
                                                                                                                                                                                                                                                                                                                                                                                              PHARMACIA & UPJOHN
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99US-0427859.
99US-0428020.
99US-0428114.
99US-0429517.
99US-0429676.
99US-0429676.
99US-0429676.
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/-ote= "Second /
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/note= "Third EC loop"
301..320
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268..29
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                                                                                                                                                                                                                               215pp; English.
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Query Match Best Local Similarity Matches 395; Conserv

Conservative

54.5**%**; 99.7**%**;

Score 2091; DB 2 Pred. No. 7e-195;

DB 22; 0;

Length Indels

396; 0;

Gaps

0

Mismatches

Sequence

396

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The invention provides human G protein coupled protein receptor (HCPR) polypeptides and polynucleotides encoding them. The polypeptides can produced by standard recombinant methodology. The polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of
                                                                                                                                                Human G protein coupled prevention, diagnosis an and immune disorders -
                                                                                                                                                                                                                                    WPI; 2000-271432/23
N-PSDB; AAZ90524.
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neurological; immune disorder; cytostatic;
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                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                   Baughn
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RESULT AAU04370

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361

mwplqemppelmkpdlftypcemslisqstrlnsys

396

AAU04370 standard;

Protein;

B

Human G-protein

coupled

receptor,

hRUP16

23-OCT-2001

(first entry)

Homo

sapiens

Inverse

G-protein e agonist;

coupled receptor; GPCR; hRUP16;

lung

cancer

25-MAY-2001

16-NOV-2000;

2000WO-US31509

17-NOV-1999; 17-NOV-1999; 17-NOV-1999; 23-DEC-1999; 23-DEC-1999; 23-DEC-1999;

99US-0166088. 99US-0166099. 99US-0166369. 99US-0171900. 99US-0171901. 99US-0171902.

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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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vafiplsnkeffknyyapngvcfplhsedtesigaqiysvaiflginlaafiiivfsygs
                                                                                                                                                                                                                                       \verb|mfrplvnlshiy| fkk f qycgyaphvrsckpntdgisslenllasii qrvfvwvvsavtcf|
                                                                                                                                                                                                                                                                                                       MFRPLMNLSHIYFKKFQYCGYAPHYRSCKPNTDGISSLENLLASIIQRVFYWVVSAVTCF
MWPLQEMPPELMKPDLFTYPCEMSLISQSTRLNSYS 722
                                     tswvvifilpinsalnpilytlttrpfkemihrfwynyrqrksmdskgqktyapsfiwve
                                                 TSWVVIFILPINSALNPILYTLTTRPFKEMIHRFWYNYRQRKSMDSKGQKTYAPSFIWVE
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99.2%;
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No. 1e-193;
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21-AUG-2000;
26-SEP-2000;
26-SEP-2000;
20-OCT-2000;
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14-MAR-2000;
14-MAR-2000;
10-APR-2000;
10-APR-2000;
10-APR-2000;
28-APR-2000;
12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a human G-protein coupled receptor (GPCR), hRUP16. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 33; Page 105-106; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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                                                                                                                                                    in the human condition, both normal and diseased.
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DB; AAS07943.
                      MIHRFWYNYRQRKSMDSKGQKTYAPSFIWVE 686
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2000US-0189258.
2000US-0199259.
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2000US-020419.
2000US-0203630.
2000US-0203630.
2000US-0216760.
2000US-0235719.
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2000US-0235719.
2000US-0235713.
2000US-0242333.
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Pred. No. 1.1e-96;
7; Mismatches 65; I
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19-MAY-2000;
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14-AUG-2000

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30-JUN-2000;
07-JUL-2000;
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2000US - 0234998
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cc (AAM99986-AAM99984) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are collated from a range of human tissues disclosed in the specification. Cc The nucleic acids, proteins, antibodies and (ant)agonists are useful cc in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone cmarrow, breast, gastrointestinal tract, liver, lung, or urogenital; cc marrow, breast, gastrointestinal tract, liver, lung, or urogenital; cc (b) immune disorders e.g. Addison's disease, allergies, autoimmune cc disease, multiple solerosis, rheumatoid arthritis and ulcerative cc olitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as wiral, bacterial, fungal cand parasitic infections.

Cc Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formative.
                                                                                 Query Match
Best Local
   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated digestive system associated polypeptide for treating, preventing and/or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection
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   182;
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 h 24.7%;
Similarity 100.0%;
82; Conservative (
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Score 948; DB 22;
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 18-APR-2000
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2000US-018658.
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2000US-021486.
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vulnerary;
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2000US-023401.
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                                                                                                                                                                                                                                                                                                                                 Query Match 23.8
Best Local Similarity 99.4
Matches 175; Conservative
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
  ABB04062
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    standard;
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Protein; 176
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XX
AC ABB04062;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polypeptide SEQ ID NO 2009.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiv
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system.

Homo

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31-JAN-2001; 2001WO-US01338.

PR 04-FEB-2000; 2000US-01186528.

PR 04-FEB-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-018874.

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PR 11-MAY-2000; 2000US-0209467.

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06-DEC-2000;
08-DEC-2000;
                 ABB10249
                                                  ABB10249 standard;
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Note: The sequence data for this
printed specification, but was ob
from WIPO at ftp.wipo.int/pub/pub
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and urcarative colitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
: The sequence data for this patent did not form p
ted specification, but was obtained in electronic
WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 1.7e-80;
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21-JUL-2000;

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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
21-NOV-2000;
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       2000US-232401P.
2000US-233064P.
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2000US-23499P.
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2000US-2518689
2000US-2518699
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2000US-2519909
2000US-2540979
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  2000US-0179065.
2000US-0180628.
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2000US-0186350.
2000US-0189874.
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12-AUG-2000
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22-AUG-2000
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18-APR-2000;
19-MAY-2000;
07-UUN-2000;
28-UUN-2000;
30-UUN-2000;
07-UUL-2000;
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2000US-0190076.
2000US-0190076.
2000US-0205515.
2000US-0216647.
2000US-02174880.
2000US-02174880.
2000US-02174890.
2000US-0217496.
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2000US-0225267.
2000US-0225266.
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2000US-0225758.
2000US-0225759.
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2000US-0225708.
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13-CCT-2000
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                              Claim 11; SEQ
                                                             Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine mot e.g. disorders associated with pregnancy and the menstrual cy
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                                                                                                                              2001-488777/53.
)B; AAS28950.
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2000US-0251856.

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10 - MAR - 2000;

11 - MAR - 2000;

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11 - AFR - 2000;

12 - MAY - 2000;

07 - JUN - 2000;

28 - JUN - 2000;

28 - JUN - 2000;

30 - JUN - 2000;
                                                                                                                                                                                                                                                                                                 Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; hyperprovascular disorder; breast; liver; cardiovascular disorder; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; gastrointestinal disorder; renal disorder; respiratory disorder; skin aging; organ transplantation; food preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU18094-AAU18152 represent novel human uterine motility-association polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                        regeneration;
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2000US-0179065.
2000US-0188628.
2000US-01886350.
2000US-018874.
2000US-0198974.
2000US-0199123.
2000US-0205515.
2000US-0205467.
2000US-0215135.
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                                                                                                                                                                            2001WO-US01308
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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Pred. No. 1.7e-80;
0; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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20-OCT-2000

20-OCT-2000

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01-NOV-2000

08-NOV-2000

17-NOV-2000

17-NO
                                                                                                                                                                             Isolated p
disorders
endocrine
Sequences AAU18282-AAU18507 represent endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases suc
                                                                                                                                                                                                                                                    WPI; 2001-451936/48
N-PSDB; AAS29573.
                                                                                                                                             Claim
                                                                                                                                                                             polypeptide for treating, preventing and/or prognosing s of the endocrine system such as reproductive disorders, e cancers and also for testing and detection e.g. diagnosis
                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                        Barash
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2000US-0241808

2000US-0244617

2000US-0246476

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of

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2000US-0216647
2000US-0217496
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2000US-022964
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2000US-0225213
2000US-0225266
2000US-0225266
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225758
2000US-0225836
2000US-0225836
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2000US-0237038
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Matches
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Best Local
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
97-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebrovascular disorders such as cerebrovascular disorders such as cerebrovascular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as sthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sumburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia; blood casqulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; neoplastic disorder; nephroma; autoimmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; vound healing; respiratory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU18666 standard;
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                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renal and cardiovascular-associated protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU18666;
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175; Conserv
 2000US-0186350.
2000US-0189874.
2000US-0199076.
2000US-0199123.
2000US-0205515.
2000US-0209467.
2000US-02113135.
2000US-0215135.
2000US-0216647.
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2000US-0184664
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No. 1.
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14-AUG-2000

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18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

01-SEP-2000

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16-SEP-2000

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18-SEP-2000

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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                   2000US-0231413
2000US-0231414
2000US-0232080
2000US-0232396
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2000US-023349
2000US-0233401
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2000US-0233063
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2000US-02344997
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2000US-0217496
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2000US-0218290
2000US-022964
2000US-0225211
2000US-0225211
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2000US-02258924
2000US-0229343
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2000US-0229314
2000US-0239343
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017-NOV-2000
diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction), blood disorders (e.g. anaemia or blood coagulation disorders),
                                          The invention relates to novel nucleic acids and polypeptides useful diagnosing, treating, preventing and/or prognosing disorders related these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which
                                                                                                                                                             preventing or prognosing electrolyte imbalance or
                                                                                                                     Claim
                                                                                                                                                                                          New polynucleotides and
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                                                                                                                                                                                                                       2001-488787/53.
DB; AAS30187.
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2000US-0251856.

2000US-0251869.

2000US-0251969.

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2000US-0254097.

2001US-0259678.
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2000US-0246523
2000US-0246525
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2000US-0246611
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                                                                                                                                                                                                                                                                 SC,
                                                                                                                     105;
                                                                                                                                                                                                                                                                                            SCI INC
                                                                                                                                                       polypeptides, useful for diagnosing, treating, g e.g. kidney, cardiovascular, blood, r neoplastic disorders, autoimmune diseases,
                                                                                                                                                                                                                                                                 Ruben
                                                                                                                  506pp;
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AAU21646
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16-MAR-2000

11-MAR-2000

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11-MAR-2000

07-JUN-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder muscular disorder; reproductive disorder; gastrointestinal disorder; bulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human neoplastic disease associated
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175; Conser
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               2000US-0189874.
2000US-0199076.
2000US-0198123.
2000US-0205457.
2000US-02014867.
2000US-0211886.
2000US-0215135.
2000US-0215487.
2000US-02174887.
2000US-0217486.
2000US-0217496.
2000US-0217496.
2000US-0210890.
2000US-0210890.
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2000US-0186350
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Pred. No. 1.7e-80;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti inflammatory;
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The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, jumnune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, are cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU21568-AAU21851 represent the novel human
                                                                                                                                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis
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                                                                                                                                                                                                                                                                                   Claim
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RESULT 1
ABB00 ABB0
XX ABB00 XX
AR ABB00 XX
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DE Huma
XX Cytc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiant; gene therapy; cancer; immune oneurological disease; infection; human; musculoskeletal system.
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (AABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and cother cancers of the adrenal gland, bone, bone marrow, breast, cother cancers of the adrenal gland, bone, bone marrow, breast, cother cancers of the adrenal gland, bone, bone marrow, breast, cother cancers of the adrenal gland, bone, bone marrow, breast, cother cancers of the adrenal gland, bone, bone marrow, breast, and control cancers e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, cullitiple sclerosis, rheumatoid arthritis and ulcerative colitis; comultiple sclerosis, rheumatoid arthritis and ulcerative colitis; comparison of the colitis of the c
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17 NOV-2000
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  Note: The sequence dat printed specification,
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                                         parasitic infections
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Claim 11; Page 1840-1841; 5507pp; English

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RESULT 1
AAB41526
ID AAB44
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XX Huma
XX Huma
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XX Wulnr
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                                               Novel nucleic acids and peptides useful for treating e.g. cancers neurodegenerative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; slergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuropr
anticonvulsant; osteopathic; antiarthritic; immunosuppressant;
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Query Match 12.6%; Score 483.5; DB 4; Lengtl Best Local Similarity 23.3%; Pred. No. 1.2e-30; Matches 144; Conservative 133; Mismatches 261; Indel:	RESULT 1 US-07-757-342D-4 US-07-757-342D-4 Sequence 4, Application US/07757342D Patent No. 6218509 Patent No. 6218509 Patent No. 6218509 FAPLICANT: IGARASHI, Masao APPLICANT: IGARASHI, Takashi NAKAMURA, Kazuto TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROUMBER OF SEQUENCES: 10 COUNTRY: US STATE: MASSACHUSETTS COUNTRY: US COUNTRY: US COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/07/757,342D FILING DATE: 10-Sep-1991 CLASSIFICATION NUMBER: 31003 REFERENCE/DOCKET NUMBER: 31003 REFERENCE/DOCKET NUMBER: 31003 REFERENCE/DOCKET NUMBER: 41226 TELEPHONE: 10617533-3400 TELEPAX: (617)523-3400 TELEPAX: (617)523-6440 TELEX: 200291 STRE UR SEQUENCE CHARACTERISTICS: LEGUTH: 506 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: Protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:	28 294.5 7.7 332 1 US-08-118-270-53 29 294.5 7.7 332 5 PCT-US93-08528-53 30 293.5 7.7 605 4 US-09-05-3-950-5 31 289 7.5 327 1 US-08-118-270-55 32 289 7.5 1480 3 US-09-19-647-7 34 286.5 7.5 1480 4 US-09-540-245A-7 35 286.5 7.5 1480 4 US-09-540-153-7 36 286.5 7.5 1480 5 PCT-US93-08528-55 37 285.5 7.4 1480 5 PCT-US91-09055-2 38 285.5 7.4 1480 5 PCT-US91-09055-2 40 285.5 7.4 1525 3 US-09-191-047-2 40 285.5 7.4 1525 4 US-09-191-047-2 41 279 7.3 1523 4 US-09-540-245A-2 42 278.5 7.3 1523 4 US-09-540-153-2 43 273 7.1 1091 3 US-08-986-485-5 44 267.5 7.0 1101 3 US-08-986-485-5 45 259.5 6.8 649 4 US-09-188-930-305
gth 696; els 79;	ROBERTS &	Sequence Sequence
Gaps 1	~	53, Appl 55, Appl 55, Appl 7, Appl 7, Appl 7, Appl 2, Appl 2, Appl 2, Appl 2, Appl 3, Appl 5, Appl 5, Appl 5, Appl 5, Appl

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RESULT 2
US-07-757-342D-6
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                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                       MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IGARASHI, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSCANPFLYAIFTKAFR 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSALNPILYTLTTRPFK 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLYAMSII---SLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQLVGSLAILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -YCGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVICMRPYIRSEN
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                                                                                                                                                                                                                                           STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                DIKE, BRONSTEIN,
                                                                                                                       #1.25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 662
                                                                                                                                549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
HNFHARKSHCSSAPRV-TNSYVLVPL
                                                                                                                                THIYLTVRNPTIVSS-----SSDTKIAKRMATLIFTDFLCMAPISFFAISASLKVPLI-
                                                                                                                                                                                                                                                                                                                                 LVV--LTTSQYKLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAG
                             YNYRORKSMDSKGOKTYAPSFIWVEM
                                                               TVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFILLSKFGCYEMQAQIYRTETSSAT
                                                                                                TITSWVVIFIL--PINSALNPILYTLTTRPFKE----MIHRF-----W
                                                                                                                                                              GSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQVEIPG
                                                                                                                                                                                                FAAALFPI----FGISSYMKVSICLPM----DIDSPLSQLYVMAL-LVLNVLAFVVICGCY
                                                                                                                                                                                                                               FIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVFSY 564
                                                                                                                                                                                                                                                                CDAAGFFTVFASELSVYTLTAITLERWHTITHAMQL----ECKVQLRHAASVMVLGWTFA
                                                                                                                                                                                                                                                                                                CQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR----TITVLILIWITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -SHIYFKKFQY--CGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31003
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Pred. No. 1.8e-30;
40; Mismatches 272;
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US-08-487-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY_AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE_POCKET NUMBER: 08/252
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS MASS11 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cheng, Shirley Vui Yen APPLICANT: Nugent, No. 5744448een Pat TITLE OF INVENTION: Human Follicle St TITLE OF INVENTION: Hormone Receptor NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                   FEATURE:
                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                      NAME/KEY: putative transmembrane region LOCATION: 350 to 370 IDENTIFICATION METHOD: similarity to other transmembrane region protein-coupled a
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: putative ami LOCATION: 1 to 349 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                     NAME/KEY: transmembrane LOCATION: 350 to 613 IDENTIFICATION METHOD: s
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: signal sequence LOCATION: -17 to -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                    IDENTIFICATION IDENTIFICATION
                                                            LOCATION:
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                                                                                 NAME/KEY:
                                                                                                                     IDENTIFICATION METHOD:
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Nugent, No. 5744448een Patrice
                                                                                                                                                                                                                                                                                                                                                                                            putative amino-terminal extracellular 1 to 349
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                                                            putative transmembrane 382 to 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)
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US-08-482-855-2
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS Version 4.0
SOPTWARE: VAX/VMS MASSII via Kermit to IB
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/482,855
FILING DATE: 07-JUN-1995
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APPLICANT: Kelton
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670, 0
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 723-13
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO:
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APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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IDENTIFICATION METHOD: protein-coupled rec
IDENTIFICATION METHOD: hydrophobic, about :
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                QWNLIRKLPPDCFKNYHDLQKLDLQNNKITSISIYAFRGLNSLTKLYLSHNRITFLKPGV 158
NKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSLEGIE------
                                                                                                                                                                                                                                                     FEDLHRLEWLIIED-NHLSRISPPTFYGLNSLILLVLMNNVLTRLPDKPLCQHMPRLH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLPQLLHCNGVDDCGNQADEDNCVVVLCQCMSLPGLELDWMKPFTSVPS-VSSNVTAMSL 98
                                                               QKVLLDIQDNINIHTIERNSFYGLSFESVILWLNKNGIQEIHNCAFNGTQ-LDELNLSDN
                                                                                                                          ---WLDLEGN-HIHNLRNLTFISCS-NLTVLVMRKNKINHLNENTFAPLQKLDELDLG-S
                                                                                                                                                                                             FSNLPKLHEIRIEKANNLLYINPEAFQNLPNLQYLLISNTGIKHLPD-----VHKIHSL 144
                                                                                                                                                                                                                                                                                                                        VLTKLRVIQKGAFSGFGDLEKIEISQNDVLEV-----IEADV 90
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Pred. No. 3.4e-30;
9; Mismatches 250;
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RESULT 5
US-07-757-342D-3
US-07757-342D-3; Sequence 3, Application US/07757342D; Patent No. 6218509; GENERAL INFORMATION:
         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
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APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY_AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MINEGISHÍ, Takashi
NAKAMURA, KAZUTO
NUMEROF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN
CUSHMAN
                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
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RESULT 6
US-07-757-342D-10
; Sequence 10, Application US/07757342D
; Patent No. 6218509
; GENERAL INFORMATION:
; GENERAL INFORMATION:
Takasan
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Best Local Similarity
Matches 149; Conserv
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              APPLICANT: IGARASHI, Masao
MINEGISHI, Takas
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEIN, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIPIMLGGWLFSTLIATMPLVG---ISNYMKVS-ICLPM---DVESTLSQVYILSILI-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITVLILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGI 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGEYNKHAQLWMESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR- 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVFVWVVSAVTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKF 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IALSSYSLKTLP----SKEKFTSLLVATLTYPSHCCAFRNLPKKEQNFSFSIFENFSKQC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOKLDE------LDLGSNKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYL 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTRLPDKPLCQHMPRLHWLDLEGNHIHNLRNLTFISCSNLTVLVMRKNKINHLNENTFAP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQNTKNLLYIEPGAFTNLPRLKYLSICNTGIRTLPDVTKISSSEF----NFILEICDNLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVV 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTVRKADNETLYSAIFEENELSGWDYDYGFC--SPKTLQCAPEPDAFNPCEDIMGYAFL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVVAFVVICACYIRIYFAVQNPELTAP-----NKDTKIAKKMAILIFTDFTCMAPISFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGQYYNHAIDWQTGSGCGAAGFFTVFASELSVYTLTVITLERWHTITYAVQLDQKLRLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVLIWLINILAIFGNLTVLFVLLTSRYKLTVPRFLMCNLSFADFCMGLYLLLIASVDSQT 426
                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                             STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                         NAKAMURA, Kazuto
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Pred. No. 1.3e-29;
35; Mismatches 233;
                                                                                                                                                                                                                 DIKE,
                                                                                                                                                                                                                                                                                                AND USE THEREOF
                                                                                                                                                                                                                    BRONSTEIN,
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REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEPAX: (200291 STRE UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENCTH: 674 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 144;
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582 LLVLFYPINSCANPFLYAIFTKTFQ 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 TFVNLLEATLTYPSHCCAFRNLPTKEQNFSHSISENFSKQCESTVRKVSN--KTLYSSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KITSISIYAFRGLNSLTKLYLSHNR-ITFLKPGVFEDLHRLEWLIIEDNHLSRISPPT-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 12.2%; Score 469; DB 4; I
Local Similarity 23.0%; Pred. No. 1.7e-29;
hes 144; Conservative 140; Mismatches 277;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                       IFIL--PINSALNPILYTLTTRPFK 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSSESNFILEICDNLHITTIPGNAFQGMNNESVTLKLYGNGFEEVQSHAF-NGTTLTSLE 178
                                                                                      RNPELMAT-----NKDTKIAKKMAILIFTDFTCMAPISFFAISAAFKVPLI-TVTNSKV 581
                                                                                                                                                                           LVG---VSNYMKVS-ICFPM---DVETTLSQVYILTILI-LNVVAFFIICACYIKIYFAV 528
                                                                                                                                                                                                                                                                                                              VGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR-TITVLILIWITGFIVAFIP 511
                                                                                                                                                                                                                                                                                                                                                                                                     CMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKENVHLEKMHNGAFRGATGPKTLDISSTKLQALPSYGLESIQRLIATSSYSLKKLPSRE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRKN-KINHLNENTFAPLQKLDELDLGSNKIENLPPLIFKDLKEL---SQLNLSYNPIQK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLERIEANAFDNLLNLSEILIQNTKNLRYIEPGAFINLPGLKYLSICNTGIRKFPDVTKV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCVPDGALR------CPGPTAGLTRLSLAYLPVKVIPSQAFRGLNEVIKIEISQID
                                                                                                                                 HQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQVEIPGTITSWVV 631
                                                                                                                                                                                                                        LSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVFSYGSMFYSV 571
                                                                                                                                                                                                                                                                    AGFFTVFASELSVYTLTVITLERWHTITYAIHLDQKLRLRHAILIMLGGWLFSSLIAMLP
                                                                                                                                                                                                                                                                                                                                                             FVLLTSRYKLTVPRFLMCNLSFADFCMGLYLLLIASVDSQTKGQYYNHAIDWQTGSGCST
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AESELSGWDYEYGFCLPKTPRCAPEPDAFNPCEDIMGYDFLRVLIWLINILAIMGNMTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYGLNSLILLVLMNNVLTRLPDKPLCQHMPRLHWLDLEGNHIHNLRNLTFISCSNLTVLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/757,342D FILING DATE: 10-Sep-1991 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QFDYLVK---LKSLSLEGIEISNIQQRMFRPLM 332
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US-07-757-342D-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 12.2%; Score 469; DB 4;
Best Local Similarity 23.0%; Pred. No. 1.8e-29;
Matches 144; Conservative 140; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200291 STRE UINFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              145
322 AESELSGWDYEYGFCLPKTPRCAPEPDAFNPCEDIMGYDFLRVLIWLINILAIMGNMTVL
                                             333 NLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVI 392
                                                                                          264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 CQCMSLPGLELDWMKPFTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDL-QNN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKAMURA, KAZUTO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IGARASHI, Masao
                                                                                       TFVNLLEATLTYPSHCCAFRNLPTKEQNFSHSISENFSKQCESTVRKVSN--KTLYSSML 321
                                                                                                                                                                                                                                                                                                                                                                   SLERIEANAFDNLLNLSEILIQNTKNLRYIEPGAFINLPGLKYLSICNTGIRKFPDVTKV 144
                                                                                                                                                                                    LKENVHLEKMHNGAFRGATGPKTLDISSTKLQALPSYGLESIQRLIATSSYSLKKLPSRE 263
                                                                                                                                                                                                              MRKN-KINHLNENTFAPLQKLDELDLGSNKIENLPPLIFKDLKEL---SQLNLSYNPIQK 298
                                                                                                                                                                                                                                                                              FSSESNFILEICDNLHITTIPGNAFQGMNNESVTLKLYGNGFEEVQSHAF-NGTTLTSLE 203
                                                                                                                                                                                                                                                                                                                      FYGINSLILLVLMNNVLTRLPDKPLCQHMPRLHWLDLEGNHIHNLRNLTFISCSNLTVLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/757,342D FILING DATE: 10-Sep-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
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                                                                                                                                    --QFDYLVK---LKSLSLEGIEISNIQQRMFRPLM 332
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US-07-757-342D-8
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                                                                                                                                                                      US-07-757-342D-8
                                                             Query Match
Best Local Similarity
Matches 134; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/07757342D Patent No. 6218509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ UD NO: 8:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA
                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
CQCMSLPGLELDWMKPFTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDL-QNN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/757,342D FILING DATE: 10-Sep-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                       LENGTH: 611 amino acids
                                                                 Conservative
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                                                               11.7%; Score 449.5; DB 4; 22.5%; Pred. No. 5.4e-28; tive 134; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                41226
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                                                                                                     Length
                                                               Indels
                                                                                                         611;
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RESULT 9
US-07-757-342D-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/07757342D
Patent No. 6218509
GENERAL IMFORMATION:
APPLICANT: IGARASHI, Masao
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                                                           APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 3103
REFERENCE/DOCKET NUMBER: 41226
                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROTEIN, DNA NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDFTCMAPISFFAISAAFKVPLI-TVTNSKVLLVLFYPINSCANPFLYAIFTKTFQ
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                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: US
                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 Water Street
TELEFAX: (617)523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                                                                                                    02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKAMURA, Kazuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINEGISHI,
                    (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EYGFC--LPKTPRCAPEPDAF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND USE THEREOF
                                                                                                                                                                                                                                            Version
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RESULT 10
US-07-741-453A-55
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                                                                                                                                                                                                                                  Sequence 55, Application US/07741453A Patent No. 6228597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                        APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSARP, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              601 TDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFIL--PINSALNPILYTLTTRPFK 654
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  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KITSISIYAFRGLNSLTKLYLSHNR-ITFLKPGYFEDLHRLEWLIIEDNHLSRISPPT-- 182
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 CNCVPDGALR-----CPGPTAGLTRLSLAYLPVKVIPSQAFRGLNEVIKIEISQID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 CQCMSLPGLELDWMKPFTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDL-QNN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 11.7%; Score 449.5; DB 4; Local Similarity 22.5%; Pred. No. 5.7e-28; les 134; Conservative 134; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIHLDQKLRLRHAILIMLGGWLFSSLIAMLPLVG---VSNYMKVS-ICFPM---DVETTL
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                                                                                                                                                                                                                                                                                                                                                                      TDFTCMAPISFFAISAAFKVPLI-TVTNSKVLLVLFYPINSCANPFLYAIFTKTFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPCEDIMGYDFLRVLIWLINILAIMGNMTVLFVLLTSRYKLTVPRFLMCNLSFADFCMGL
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  WASHINGTON,
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N FOR SEQ ID NO: 7:
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                                      CUSHMAN DARBY & CUSHMAN
STREET, N.W.
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REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEFX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1; MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 795 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NLSELLIQNTKNLLYIEPGAFTNLPRLKYLSICNTGIRTRATHCGLPDVTKISSSEF--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGPRAGLARLSLTYLPVKVIPSQAFRGLNEVVKIEISQSDSLERATHCGRIEANAFDNLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.5%; Score 441; DB 4; Length 795; Local Similarity 22.2%; Pred. No. 3.6e-27; ses 157; Conservative 131; Mismatches 230; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U. FILING DATE: 19911015
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GWLFSTLIATMPLVG---ISNYMKVS-ICLPM---DVESTLSQVYILSILIRATHCGLNV
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                                                 IWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFL-----GINL
                                                                                                                                                              S-----FRCVRPGKCRTITVLIL 499
                                                                                                                                                                                                                      LLTSRYKLTVPRFLMCNLSFADFCMGLYLLLIASVDSQTKGQYYNHAIDW-RATHCGQTG
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                                                                                                      SGCGAAGFFTVFASELSVYTLTVITLERWHTITYAVQLDQKLRLRHARATHC-GIPIMLG
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US-07-741-453A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
TITLERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 764 amino acid
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REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                              142 PDLTKVYSTDIFFILEITDNPYMTSIPVNAFQGLCNETLTLKLYNNGFTSVQGY-----
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ZIP: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                             CQCMSLPGLELDW----MKPFTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISFFAISAAFKVPLI-TVTNSKILLVLFYPVNSCANPFLYAIFTKAFQ 718
                                                                                                                                                                                          IDLTLQQLESHSFY---NLSKVTHIEIRNTRNLTYIDPDALKELPLLKFLGIFNTGLKMF 141
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ilarity 22.9%; Pred. No. 5e-27;
Conservative 128; Mismatches 2
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(02) 822-0944
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
                                                                                                                                  IIEDNHLSRISPPTFYGL-NSLILLVLMNNVLTRLPDKPLCQHM
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                       -----SCSNLTVLVMRKNKINHLNE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND APPLICATIONS OF THESE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                    284;
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US-07-741-453A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                    TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                  REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 861-3000
                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULLS, PAUL N.
REGISTRATION NUMBER: 16773
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VASSART, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: UPPLICATION NUMBER: UPPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1615 L STREET, N.W. CITY: WASHINGTON, D.C.
                                                                              TELEFAX:
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SUCH RECEPTORS POLYPEPTIDES

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RESULT 13
US-07-757-342D-5
; Sequence 5, Application U
; Patent No. 6218509
; Patent INFORMATION:
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Best Local Similarity
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TOPOLOGY: 1ii
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                627 TSWVVIETL--PINSALNPILYTLTTRPFKE----MIHREWYNYRQRKSMDSKGQK 676
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TYPE: A
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                APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          SNSKILLVLFYPLNSCANPFLYAIFTKAFQRDVFILLSKFGICKRQAQAY--RGQR 710
                                                                                                                                                                                                                                                                                                                                                       IYITVRNPQY-----NPGDKDTKIAKRMAVLIFTDFICMAPISFYALSAILNKPLI-TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR-TITVLILIWITGFI 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVLLI---LLTSHYKLNVPRFLMCNLAFADFCMGMYLLLIASVDLYTHSEYYNHAIDWQTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNLSHIYFKKFQY--CGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LALLPLVG----ISSYAKVSICLPM---DTETPLALAYIMSV-LVLNIVAFVIVCCCYVK 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NTFA----PLQ----KLDELDL------GSNKIENLPPLI----FKDLKELSQ 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CECHQ----EEDFRVTCKDIQRIPSLPPSTQTLKLIETHLRTIPSHAFSNLPNISRIYVS
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    ADDRESSEE:
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DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 438; DB 4; Length 764; 22.8%; Pred. No. 6e-27; tive 130; Mismatches 283; Indels 1
                                                                                                                                                                             US/07757342D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EGIEISNIQQRMFRPL 331
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID

US-07-757-342D-5
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                        448 THCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR-TITVLILIWITGFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                    PGCNTAGFFTVFASELSVYTLTVITLERWYAITFAMRLDRKMRLRHACAIMVGGWVCCFL
                                                                                                FVLLI--LLTSHYKLNVPRFLMCNLAFADFCMGMYLLLIASVDLYTHSEYYNHAIDWQTG
                                                                                                                                     FVICMRPYIRSENKLYAMSII---SLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMES
                                                                                                                                                                           EETLQAFDSHYDYTICGDSEDM-VCTPKSDEFNPCEDIMGYKFLRIVVWFVSLLALLGNV
                                                                                                                                                                                                           MNLSHIYFKKFQY--CGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNI 389
                                                                                                                                                                                                                                                      VNALNSPLHQEYEENLGDSIVGYKEKSKFQDTHNNAHYYVFFEEQEDEIIGFGQELKNPQ
                                                                                                                                                                                                                                                                                            RNTWTLKKLPLSLSFLHLTRADLSYPSHCCAFKNQKKIRGILESLMCNESSMQSLRQRKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLQNNKITSISIYAFRGLNSLTKLYLSHNR-ITFLKPGVFEDLHRLEWL------ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CECHQ----EEDFRVTCKDIQRIPSLPPSTQTLKLIETHLRTIPSHAFSNLPNISRIYVS
                                                                                                                                                                                                                                                                                                                                                                                                               -AFNGTKLDAVYLNKNKYLTVIYKDAFGGVYSGPSLLDVSQTSVTALPSKGLEHLKELIA
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
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Pred. No. 7.2e-27;
9; Mismatches 284
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Gaps

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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                            157
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TOPOLOGY: li
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
FILING DATE: 19911015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
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                                                                                                                                                                         PQLLHCNGVDDCGNQADEDNCVVVLCQCMSLPGLELDW---MKPFTSVPSVSSNVTAMSL 98
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                        GVFEDLHRLEWL-
                                                             IETQLKTIPSRAFSNLPNISRIYLSIDATLQRLESHSFYNLSKMTHIEIRNTRSLTSIDP 119
                                                                                                                                        PPLLHLALLLALPRSLGGKGCPSPPCECHQ----EDDFRVTCKDIHRIPTLPPSTQTLKF 59
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                                                                                                    QWNLIRKLPPDCFKNYHDLQKLDLQ-NNKITSISIYAFRGLNSLTKLYLSHNR-ITFLKP 156
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                                                                                                                                                                                                                                                                                                                                                                                                                      764 amino acids
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LIBERT, FREDERIC
DUMONT, JACQUES
                                                                                                                                                                                                                    11.2%; Score 430; DB 4; Length 764; ilarity 21.3%; Pred. No. 2.6e-26; Conservative 139; Mismatches 286; Indels 1
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
62
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    ----IIEDNHLSRISPPTFYGL-NSL 189
                                                                                                                                                                                                                      Indels 170;
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US-07-741-453A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICATION NUMBER: US/07, FILING DATE: 19911015 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL N.
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DUMONT, APPLICANT: VASSART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                           CITY: WASHINGTON,
                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICLPM---DTETPLALAYIILVLL-LNIVAFIIVCSCYVKIYITVRNPQY-----NPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTVITLERWYAITFAMRLDRKIRLRHAYAIMVGGWVCCFLLALLPLVG----ISSYAKVS 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTELTLEKYICIVYPERCVRPGKCR-TITVLILIWITGEIVAFIPLSNKEFEKNYYGTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I--SLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQLVGSLAILSTEVSVLL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDMVCTPKSDEFNPCEDIMGYKFLRIVVWFVSLLALLGNVFVLIV--LLTSHYKLTVPRF 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVICMRPYIRSENKLYAMSI 409
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                                                                                                                                                                                                                                                                                                  CUSHMAN DARBY
                                                                                                                                                                                                                                                             D.C.
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                      GILBERT
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                                                                                                                                                                                                                                                                                                CUSHMAN
                                                                                                                    Version
                                                                                                                        #1.25
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; TELEPHONE: (202) 861-3000
; TELEPAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 56.
; SEQUENCE CHARACTERISTICS:
; SENGTH: 792 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-741-453A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
608 GHCGLNVVAFIIICACYIKIYFAVQNPELMAT----NKDTKIAKKMAVLIFTDETCMA
                                                                                                                     551 ---GINLAAFIIIVESYGSMEYSVHQSAITATEIRNQVKKEMILAKREFFIVETDALCWI 607
                                                                                                                                                                                                                                                                                                                                    438 PIGHC--GLLTSHYKLTVPRFLMCNLSFADFCMGLYLLLIASVDAQTKGQYYNHAIDWPI 495
                                                                                                                                                                                                                                                                                                                                                            393 ----CMRPYIRSENKLYAMSII--SLCCADCLMGIYLFYIGGFDLKFRGEYNKHAQLW-- 444
                                                                                                                                                                                                                                                                                                                                                                                                                       378 GYDYGPIGHCGFCSPKTLQCAPEPDAFNPCEDIMGYDFLRVLIWLINILAIMGNVTVLFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 FRNLPPIGHCGTKEONFSFSIFKNFSKOCESTARRPNNETLYSAIFAESELSDWDPIGHC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 GHCGLPSYGLESIQTLIATSSYSLKKLPSREKFTNLLDATLTYPSHCC------A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 ---NLPPLIFKDLKEL----SQLNLSYNPIQKIQANQFDYLVKLKSLSLEGIEISNIQQRM 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 TITVLILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFL-- 550
                                                                                                                                                                                                                                                    496 GHCGQTGNGCSVAGFFTVFASELSVYTLTVITLERWHTITYAIQLDQKLRLRHAPIGHC- 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 --IIEDNHLSRISPPTFYGLNSLILLVLMNNVLTRLPDKPLCQHMPRLHWLDLEGN---- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 NLSEILIQNTKNLVYIEPGAFTNLPRLKYLSICNTGIRKPIGHCGLPDVTKIFSSEFNFI 176
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                                                                                                                                                                 GIPIMLGGWLFSTLIAMLPLVG----VSSYMKVSICLPM---DVETTLSQVYILTILIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GY-----APHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVI-- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRPL-----MNLSHIYEKKFQ-------YC 345
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                                                                                                                                                                                                                                                                                             ----MESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYP------FRCVRPGKCR 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPRAGLSRISLTYLPIKVIPSQAFRGLNEVVKIEISQSDSLEPIGHCGKIEANAFDNLL 116
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Search completed: September 5, 2002, 09:00:03 Job time: 9128 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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FRGLNSLTKLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVL 194 KLKEM----PVQQMEEDLSKLMIGDNLLNLTSTTFSATYYDKVTYLDLSRNHLTEIPIYS

CLEGQFRCRK-SFCINQTKVCDGTVDCLQGMWDENNCRYWCPHGQAICQCEGVTMDCTGQ 546

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CSLGYFPCGNITKCLPQLLHCNGVDDC-GNQADEDNCVV-----VLCQC----MSLPGL 75

603 135 547

FQNMWKLTHLNLADNNITSLKNG----

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	Scc Pre	ceptor - great pond snail tagnalis (great pond snail) #sequence_revision 06-Jan-1995 Eren, E.R.; Planta, R.J.; Cox, l L Data Library, June 1993 rotein-coupled receptor with LD: \$40241 Y MA TENN TENN S40241 PENN EMBL:23104; NID:9438128; PID:9; pond snail LDL receptor relate n-coupled receptor; transmembrai receptor ligand-binding repeat receptor ligand-binding repeat L receptor ligand-bind	ALIG	B36665 A36665 A36665 T413953 T423852 T13887 T13887 T13887 T15864 A51866 A51866 A51866 A51866 A51866 A51866 A51866 A51866 A51866
	re 832; D d. No. 7.7 Mismatches	pond snail t pond snail sion 06-Jan-1995 #text_change 15- sion 06-Jan-1995 #text_change 15- sion 06-Jan-1995 #text_change 15- nata, R.J; Cox, K.; Burke, J.F.; June 1993 receptor with LDL-binding motifs receptor with LDL-binding motifs receptor related G protein-coup t. receptor-related G protein-coup for: transmembrane protein d-binding repeat homology <ldl1> nd-binding repeat homology <ldl3 <ldl1="" <ldl3="" and-binding="" homology="" repeat=""> and-binding repeat homology <ldl3 <ldl1="" and-binding="" homology="" repeat="" repeat<="" td=""><td>ALIGNMENTS</td><td></td></ldl3></ldl3></ldl1>	ALIGNMENTS	
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Follitropin receptor - sheep
N;Alternate names: follicle stimulating hormone receptor
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Feb-194 *sequence_revision 03-Feb-1994 *text_change 21-Jan-:
C;Accession: JC1493; I47080
R;Khan, H; Yarney, T.A.; Sairam, M.R.
Biochem. Biophys. Res. Commun. 190, 888-894, 1993
A;Title: Cloning of alternately spliced mRNA transcripts coding for variancession: JC1493
A;Reference number: JC1493; MUID:93176195
A;Recession: JC1493
A;Molecule type: mRNA
A;Residues: 1-695 KHAN-
A;Starney, T.A.; Sairam, M.R.; Khan, H; Ravindranath, N.; Payne, S.; Seingle, T.A.; Sairam, M.R.; Khan, H; Ravindranath, N.; Payne, S.; Seingle, Coloring and expression of the ovine testicular follicular follicular per lumber: I47080; MUID:93351750
A;Reference number: I47080; MUID:93351750
A;Residues: 1-695 KYAR-
A;Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885
                                                                        C;Genetics:
A;Gene: FSH-R
C;Superfamily: glyc
C;Keywords: G prote
F;71-95/Domain: leu
F;191,199/Binding s
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Matches 168
                                                                        Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein; keywords: G protein-coupled receptor; glycoprotein; transmembrane protein; fkeywords: G protein-coupled receptor; glycoprotein repeat homology CLRR>;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR>;191,199/Binding site: carbohydrate (Asn) (covalent) #status predicted
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13.1%;
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Conservative 13
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Score 501; DB 2;
Pred. No. 6.5e-26;
0; Mismatches 245;
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                            Length 695;
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Score Pred.

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ELPNDVFQGASGPVILDISRTRIRSLPSYGLENLKKLRAKSTYHLKKLPSLEKFVTLVEA
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       glycoprotein hormone receptor; leuc
: leucine-rich alpha-2-glycoprotein
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                                                                        NID:g404671; PIDN:AAC37324.1; PID:g404672
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G protein-coupled receptor FEX - mouse
G:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-Ma;
C:Accession: JG0193
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Blochem. Biophys. Res. Commun. 254, 273-279, 1999
A;Title: Identification of a novel seven-transmembrane receptor with |
A;Reference number: JG0193; MUID:99121227
A;Accession: JG0193; MUID:99121227
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24.6%;
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                                                          110;
                                                      Score 490; DB 2;
Pred. No. 4.8e-25;
0; Mismatches 263;
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              A;Cross-references: GB:S70150; NID:g546896; PIDN:AAB30854.1; PID:g546897
A;Experimental source: testis
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein
C;Keywords: glycoprotein; hormone receptor; transmembrane protein
C;Keywords: glycoprotein; hormone receptor; transmembrane protein
F;56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
                                                                                                                                                                                        R;Robert, P.; Amsellem, S.; Christophe, S.; Benifla, J.L. Biochem. Biophys. Res. Commun. 201, 201-207, 1994 A;Title: Cloning and sequencing of the equine testicular A;Reference number: JC2237; MUID:94256980 A;Accession: JC2237
                                                                                                                                                                                                                                                                                  C;Species: Equus caballus (domestic horse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
C;Accession: JC2237; JC2370
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A; Residues: 1-694 < ROB>
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F:146-169/Domain: 1
F:17-193/Domain: 1
F:194-218/Domain: 1
F:366-386/Domain: t
F:368-420/Domain: t
F:443-464/Domain: t
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F:485-507/Domain: t
F:528-549/Domain: t
F:573-596/Domain: t
F:508-629/Domain: t
F:5191,199,268,293/B
RESULT 6
JC4301
follitropin 1
N;Alternate 1
C;Species: St
C;Date: 16-NC
C;Accession:
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;608-629/Domain: transmembrane
;191,199,268,293/Binding site:
  Accession:
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                       ppin receptor - pig
ss: Sus scrofa domestica (domestic pig)
16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
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                                                                                                                                                                                                                                                                                                                                           YLTVRNPNIVSS-----SSDTKIAKRMAILIFTDFLCMAPISFFAISASLKVPLI-TVS
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Pred. No. 8.2e-25;
30; Mismatches 246;
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A; Map position: 3 q2.2-q2.3
C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein F; 1-365/Domain: follicle-stimulating hormone binding #status predicted <HOB> F: 70-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR> F: 79-94/Domain: transmembrane #status predicted <TM1> F: 388/Domain: transmembrane #status predicted <TM2> F: 489-420/Domain: transmembrane #status predicted <TM3> F: 443-464/Domain: transmembrane #status predicted <TM4> F: 528-549/Domain: transmembrane #status predicted <TM5> F: 573-596/Domain: transmembrane #status predicted <TM6> F: 573-596/Domain: transmembrane #status predicted <TM5> 
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C;Genetics:
A;Gene: fshr
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A; Title: The porcine follitropin receptor: A; Reference number: JC4301; MUID:96011644
A; Recession: JC4301
A; Molecule type: mRNA
A; Residues: 1-694 < REM>
A; Cross-references: GB:L31966
A; Cross-references: GB:L31966
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FIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLS | ::| | ::|| | ::|| ::|| ::||
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                                                                                                                   LILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAA
                                                                                                                                                                                                         INWOTGAGCDAAGFFTVFASELSVYTLTAITLERWHTITHAMQL----
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70; Conservative
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Pred. No. 1.1e-24;
6; Mismatches 255;
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A;Cross-references: GB:S81198; NID:g245344; PIDN:AAB21415.1; PID:g245345 A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:81117, NCBIN:81119, R;Davis, D; Liu, X.; Segaloff, D.L. Mol. Endocrinol. 9, 159-170, 1995.

Mol. Endocrinol. 9, 159-170, 1995.
A;Fitle: Identification of the sites of N-linked glycosylation on the follower is annotation; glycosylation sites (C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: receptor that mediates the biochemical effects of follitropin (;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone receptor: p.1-15/Domain: signal sequence #status predicted <SIC>
F;16-962/Product: follitropin receptor #status predicted <MAT>
F;16-366/Domain: extracellular hormone binding #status predicted <EHB>
F;56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;96-120/Domain: leucine-rich alpha-2-glycoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:367-387/Domain: transmembrane #status predicted <TM1>
F:368-7-387/Domain: transmembrane #status predicted <TM2>
F:443-465/Domain: transmembrane #status predicted <TM3>
F:486-508/Domain: transmembrane #status predicted <TM4>
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A; Residues: 1-692 <HEC>
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A;Accession: A41729
A;Status: preliminary
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Mol. Endocrinol.
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A; Residues: 1-69
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transmembrane #status predicted <TM5>
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                                                                                                                                                                            THIYLTVRNPTIVSS-----SSDTKIAKRMATLIFTDFLCMAPISFFAISASLKVPLI-
                                                                                                                                                                                                                     GSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQVEIPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMEASLTYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQRVSLIDDEPSYGK 323
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A;Cross-references: GB:M29525; NID:g164528; PIDN:AAA31062.1; PID:g164529 C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; membrane F;1-27/Domain: signal sequence #status predicted <SIG> F;28-696/Product: lutropin-choriogonadotropic hormone receptor #status predicted <MAT F;99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR> A; Title: Cloning and sequencing of porcine LH-hCG A; Reference number: A41344; MUID:89332517 A; Accession: A41344 N;Alternate names: luteinizing hormone-choriogonadotropin receptor C;Species: Sus scrofa domestica (domestic pig) C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jan-2000 A; Molecule type: mRNA A; Residues: 1-696 <LOO> R; Loosfelt, H.; Misrahi, Science 245, 525-528, 19 C; Accession: lutropin-choriogonadotropin receptor precursor (splice form A) -A41344 hi, M.; Atger, M.; Salesse, 1989 R.; receptor cDNA: ٧u Hai-Luu Thi, M.T.; Jolivet, variants lacking tra pig

Matches

144;

Conservative

Local Similarity

12.6%; 133;

Score 481.5; DB 2 Pred. No. 1.3e-24; Mismatches

DB 2;

Indels Length 696;

79;

Gaps

17;

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follitropin receptor precursor - crab-eating macaque
N;Alternate names: follicle-stimulating hormone receptor (FSHR)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0898; S36452
R;Gromoll, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 196, 1066-1072, 1993
A;Title: Molecular cloning of the testicular follicle stimulating hormone receptor of the A;Reference number: JN0898; MUID:94071854
A;Accession: JN0898; 
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JN0898
follitropin
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RESULT 10
QRHUFT
follitropin

follitropin receptor precursor - human
N;Alternate names: follicle stimulating hormone receptor (FSHR)
N;Contains: follitropin receptor precursor long splice form; fo
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 06-Sep-1996 #text_change
C;Accession: I57661; I56448; PC1147; S30560; I57672; JN0122

R;Gromoll, J.; Dankbar, B.; Gudermann, T. Mol. Cell. Endocrinol. 102, 93-102, 1994 Nol. Cell. Characterization of the 5' flanking A;Reference number: I57661; MUID:95011044

region

of

the

human

follicle-stimulating

22-Jun-1999

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F;367-387/Domain: transmembrane #status predicted <TM1>
F;399-421/Domain: transmembrane #status predicted <TM2>
F;444-465/Domain: transmembrane #status predicted <TM3>
F;486-508/Domain: transmembrane #status predicted <TM4>
F;529-550/Domain: transmembrane #status predicted <TM5>
F;529-550/Domain: transmembrane #status predicted <TM6>
F;574-597/Domain: transmembrane #status predicted <TM6>
F;609-630/Domain: transmembrane #status predicted <TM6>
F;609-630/Domain: transmembrane #status predicted <TM6>
F;191,199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted F;555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre
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VPLI-TVSKAKILLVLFYPINSCANPFLYAIFTKNFR
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                                                VEIPGTITSWVVIFIL - - PINSALNPILYTLTTRPFK
                                                                                                                                                                                                                                                                                                  MESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR-----TITVLIL
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                                                                                         ICGCYTHIYLTVRNPNIVSS-----SSDTRIAKRMAMLIFTDFLCMAPISFFAISASLK
                                                                                                                                 IVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQ
                                                                                                                                                                            GWIFAFAAALFPI----FGISSYMKVSICLPM---DIDSPLSQLYVMSL-LVLNVLAFVV
                                                                                                                                                                                                                  IWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFII
                                                                                                                                                                                                                                                             QTGAGCDAAGFFTVFASELSVYTLTAITLERWHTITHAMQL-----DCKVHVRHAASVMVM
                                                                                                                                                                                                                                                                                                                                              IVL-----VTLTTSQYKLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDW
                                                                                                                                                                                                                                                                                                                                                                                        FVICMRPYIRSENKLYAMSI----ISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQKVLLDIQDNINIHTIERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQ-LDELNLSD
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AREASUMES, 273, 4800 573199, kth://doi.org/10.11.plD/g685037
RECEMBOLL J. REAG. P. | Holtprove:Crex. H. | Meschlag. E. | Gudermann. T. J. | No. | Endocation. 17, 25-271, 1940 |
RECEMBOLL J. REAG. P. | Holtprove:Crex. H. | Meschlag. E. | Gudermann. T. J. | No. | Endocation. | T. | Godermann. T. |
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Status: translated from GB/EMBL/DDBJ
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C; Accession: JE0176

#sequence_revision 10-Jul-1998

#text_change

orphan G protein-coupled receptor precursor C; Species: Homo sapiens (man)

RESULT JE0176

Biochem. Biophys. Res. Commun. 247, 266-27 A; Title: Identification and cloning of an A; Reference number: JE0176; MUID:98308104

orphan

G

protein-coupled

receptor of

the gl Caskey, C.T.;

Liu,

Ö

R;McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Biochem. Biophys. Res. Commun. 247, 266-270, 1998

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F;486-508/Domain: transmembrane #status predicted <TM4>
F;529-550/Domain: transmembrane #status predicted <TM5>
F;529-550/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM6>
F;609-630/Domain: transmembrane #status predicted <TM6>
F;191/199/293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted F;555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre
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                                                                                                                                              AFAAALFPI----FGISSYMKVSICLPM----DIDSPLSQLYVMSL-LVLNVLAFVVICGC
                                                                                                                                                                               GFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVFS
                                                                                                                                                                                                                                                    HCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR-----TITVLILIWIT
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                                                                         YIHIYLTVRNPNIVSS---
                                                                                                      YGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQVEIP
                                                                                                                                                                                                                                                                                           VLVI--LTTSQYKLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGA
                                                                                                                                                                                                                                                                                                                                                                  RGFDMTYTEFDYDLCNEVVDV-TCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNII
-TVSKAKILLVLFHPINSCANPFLYAIFTKNFR
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                                                                       ---SSDTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLI
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A;Residues: 1-907 <MCD>
A;Cross-references: GB;AF062006; NID:g3366801; PIDN:AAC28019.1; PID:g3366802
C;Comment: This protein is a receptor for a novel class of glycoprotein ligands.
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F;768-791/Domain:
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F;594-616/Domain:
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F;1-21/Domain: signal sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLGYFPCGNIT-----KCLPQLLHCNGVDDCGNQADEDNCVVVLCQCMSLPGLELDWMKP
                                                                                                                                                                                                                          FGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLTLAALERGFSVKYSAKFETKAPFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEF-PTAIRTLSNLKELGFHSNNI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYVPPSCFSGLHSLRHLWLDDNALTEIPVQAFRSLSALQAMTLALNKIHHIPDYAFGNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTYIPKGAFTGLYSLKVL--MLQNNQLRHVPTEA-----LQNLRSLQSLRLDANHI 150
SFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSK
                                    KFLSLLQVE-IPGTITSWVVIFILPINSALNPILYTLTTRPFKEMIHRF-----WYNYR
                                                                                                          NLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVV
                                                                                                                                               LKVIILLCALLALTMAAVPLLG----GSKYGASPLCLPLPFGEPSTMG----YMVALIL-L
                                                                                                                                                                                 ITVLILIW-ITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGI 552
                                                                                                                                                                                                                                                                                                TIAVLALTC -- NALVTSTVFRSPLYISPIKLL -- -IGVIAAVNMLTGVSSAVLAGVDAFT
                                                                                                                                                                                                                                                                                                                                                                         LHKKDAGMFQAQDERDLEDFLLDFEEDLKALHSVQCSPSPGPFKPCEHLLDGWLIRIGVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIYFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANLESTITIGAQISSIPQTVCNQLPNLQVLDLSYNLLEDLPS--FSVCQKLQKIDLRHNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNLTVLVMRKNKINHLNENTFAPLQKLDELDLGSNKIENLPPLIFKDLKELSQLNLSYNP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSIPEKAFVGNPSLITIHFYDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLT--GT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTSVPSVSSNVTAMSLQW----NLIRKLPPDCFKNYHDLQKLDLQNNKITSISIYAFRGLN 139
                                                                         NSLCFLMMTIAYTKLYCNLDKG----
                                                                                                                                                                                                                                                           RGEYNKHAQLWMESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCRT
                                                                                                                                                                                                                                                                                                                                   VVS--AVTCFGNIFV---ICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYEIKVDTFQQLLSLRSLNLAWNKIAIIHPNAFSTLPSLIKLDLSSNLLSSFPITGLHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQKIQANQFDYLVKLKSLSLEGIEISNIQQRMFRPLMN----
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195; Conservative
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n: transmembrane #status predicted <TM1>
n: transmembrane #status predicted <TM2>
n: transmembrane #status predicted <TM3>
n: transmembrane #status predicted <TM4>
n: transmembrane #status predicted <TM6>
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n: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --------QHMPRLHWLDLEG-NHIHNLRNLTFISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %; Score 476.5;
%; Pred. No. 3.96
134; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              ----APHVRSCKPNTDGISSLENLLASIIQRVFVW 378
                                                                         -DLENIWDCSMV--KHIALLLFTNCILNCPVAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9e-24;
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R; Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, Biochem. Biophys. Res. Commun. 275, 121-128, 2000 A; Title: Molecular cloning, functional characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    follitropin receptor precursor - newt
N;Alternate names: follicle-stimulating hormone receptor
C;Species: Cynops pyrrhogaster (newt)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change
C;Accession: JC7361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;370-389/Domain: transmembrane #status predicted <TM1>
F;402-424/Domain: transmembrane #status predicted <TM2>
F;447-468/Domain: transmembrane #status predicted <TM3>
F;449-511/Domain: transmembrane #status predicted <TM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F; 489-511/Domain: F; 532-553/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;18-359/Domain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: This protein, containing in and thyroid stimulating hormone.
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A; Cross-references: DDBJ:AB005587
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Best Local S
Matches 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNSTELREVLTKVTVIPKAAFSGFEDVENIEISQNDVLKTIEANVFSHLPKLREIRIEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGCHPVCRCLNRVFTC------QESHVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPCGNITKCLPQLLHCNGVDDCGNQADEDNCVVVLCQCMSLPGLELDWMKPFTSVP-SVS 90
                                                                                                                                     LGSN-KIENLPPLIFKD-----LKELSQLNLSYNP-----IQKIQANQFDYLVKLKSLS
                                                                                                                                                                                                                                                                      QHMPRLHWLDLEGN-HIHNLRNLTFISCSNLTVLV-MRKNKINHLNENTFAPLQKLDELD
                                                                                                                                                                                                                                                                                                                                            NNLVYIDPDAFQNLPSLKYLLISNTGIQLV--PAVSKIRS-----FHSVL-----
                                                                                                                                                                                                                                                                                                                                                                                                               NRITFLKPGVFEDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLMNNVLTRLPDKPLC
          --LEGIE------ISNIQQRM--FRPLMN---
                                                                      LSDNQRLEKLPDQVFQGATGPVILDISRTRIHFLPNNGIENIKKFRARFNYYLKKLPPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
163; Conserv
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Pred. No. 3.3e-
5; Mismatches
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| <TM5>
| <TM6>
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signal transduction pa
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KFAELIEANLTYPSHCCAFANRERKKSEMHPICNKSFGKHDSAEKPEDKNLRRFSNEDYL

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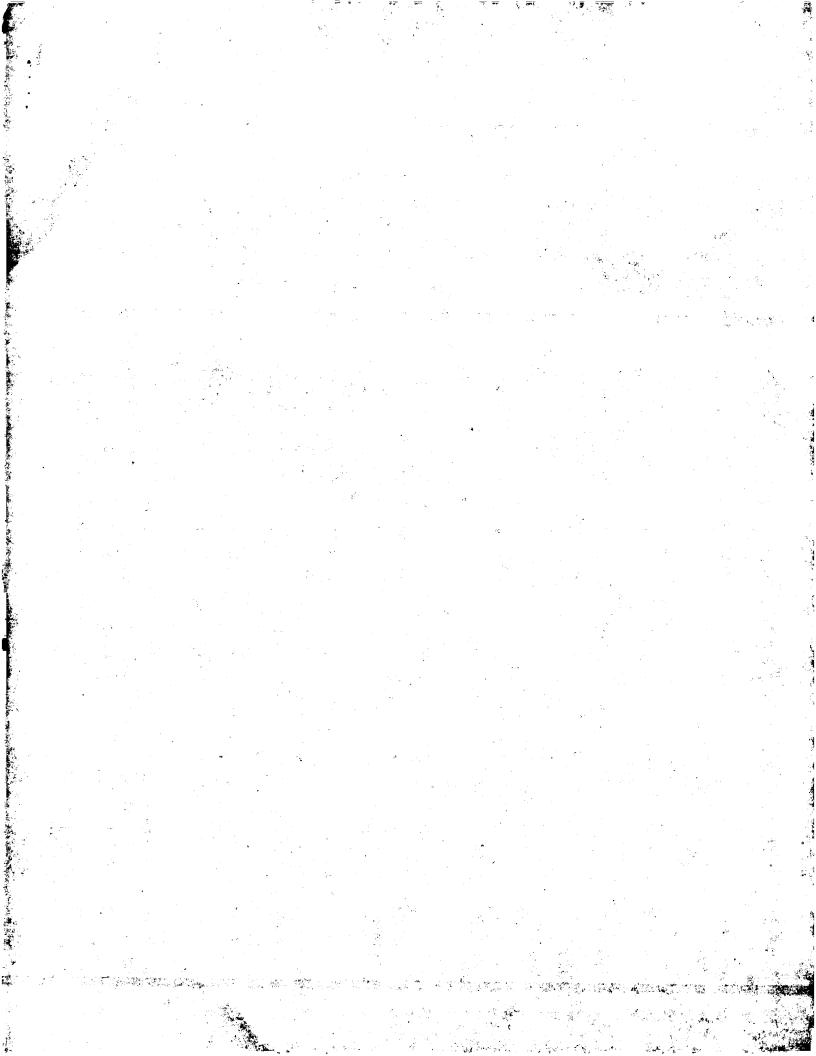
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A;Cross-references: GB:M81310; GB:M81318; NID:g198811; PIDN:AAA39432.1; PID:g198812
A;Note: sequence extracted from NCBI backbone (NCBIN:84064, NCBIP:84066)
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repe
C:Keywords: G protein-coupled receptor; transmembrane protein
F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
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N;Alternate names: luteinizing hormone-choriogonadotropin receptor
C;Species: Mus musculius (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-C;Accession: A42395
R;Güdermann, T; Birnbaumer, M; Birnbaumer, L.
J. Biol. Chem. 267, 4479-4488, 1992
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A; Molecule type: mRNA
A; Residues: 1-700 <GUD>
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A; Title: Evidence for dual coupling of the murine luteinizing hormone receptor to mone receptor expressed in L cells.
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                                                     TFAPLQKLDELDLGSNKIENLP------PLIFKDLKELSQL------NLSY-
                                                                                                       ITTIPGNAFQGMNNESITLKLYGNGFEEVQSHAF----NGTTLISLELKENIYLEKMHSG
                                                                                                                                                       LTRLPDKPLCQHMPRLHWLDLEGNHIHNLRNLTFISCSNLTVLVMRKNKIN----HLNEN
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Pred. No. 6.2e-24;
1; Mismatches 271;
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A; Title: Expression of the LH/CG receptor gene in rat ovarian tiss A; Reference number: 157668; MUID:92347804
A; Accession: 177463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luteinizing hormone/chorionic gonadotropin receptor - rat
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2 C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein F;153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
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A; Residues: 1-700 < RES>
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                                                                            LEKMHSGAFQGATGPSILDISSTKLQALPS-
                                                                                                                                                                                                                                                                                   IQNTKNILLYIEPGAFTNLPRLKYLSICNTGIRTLPDVTKISSSEF----NFILEICDNLH 164
                                                                                                                                                                                                                                                                                                                                      LSHNR-ITFLKPGVFEDLHRLEWLIIEDN-----HLSRISPPTFYGLNSLILLVLMNNV 198
                                                                                                                                                                                                                                                                                                                                                                                           PGPRAGLARLSLTYLPVKVIPSQAFRGLNEVVKIEISQSDSLERIEANAFDNLLNLSELL
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Pred. No. 7.2e-24;
35; Mismatches 233;
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C:Keywords: alternative splicing; G protein coupled receptor; glycoprotein; F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>F:202-226/Domain: transmembrane #status predicted <TM1>F:308-389/Domain: transmembrane #status predicted <TM2>F:400-422/Domain: transmembrane #status predicted <TM3>F:448-61/Domain: transmembrane #status predicted <TM3>F:448-61/Domain: transmembrane #status predicted <TM5>F:575-598/Domain: transmembrane #status predicted <TM6>F:575-598/Domain: transmemb
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F;103,178,199,295,303,317/Binding site: carbohydrate (Asn)
F;647,648/Binding site: palmitate (Cys) (covalent) #status
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C; Superfami
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A; Residues: 27-32, 'LX', 35-37 < ROC>
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Best Local Similarity 30.0%;
Matches 205; Conservative 11
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                                                           LGFVSLAGARADDQVYAWIAVFVLPLNSATNPVIYTLSTAPFLGNVRKRANRFRKSFIHS
                                                                          VKFLSLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPF-
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   FTGDTKHSYVDDGTTHSYCEKKS
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%; Pred. No. 4.1e-43;
114; Mismatches 240
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FSHR_CHICK
P79763; 090
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01-NOV-1997
16-OCT-2001
Follicle st
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YOU S., Bridgham J.T., Foster D.N., Johnson A.L.;

YOU S., Bridgham J.T., Johnson A.L.;
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MEDLINE-974/3503; PubMed-9332357;
Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Mizuno S.;
"The cDNA cloning and transient expression of a chicken gene en a follicle-stimulating hormone receptor.";
Gene 197:121-127(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                             DOMAIN
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                                                                                                                                   Phosphorylation;
SIGNAL 1
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
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InterPro; IPR001611;
InterPro; IPR000372;
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-NOV-1997 (Rel. 35, Created)
-NOV-1997 (Rel. 35, Last sequence update)
-OCY-1997 (Rel. 40, Last annotation update)
llicle stimulating hormone receptor precu
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SUBCELLULAR LOCATION: Integral membrane protein.
SYMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLIFSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
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U51097; AAC60030.1;
P23945; IXUN.
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GCR_1137;
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;tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;tazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
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EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).
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                                                                         VFVWVVSAVTCFGNIFVICMRPYIRSENKLYAMSII--SLCCADCLMGIYLFVIGGFDLK
                                                                                          KRKHRRSAAEDYISHYGTRFGPVENEFDYGLCNEVVDFVCSPKPDAFNPCEDIMGYNVLR
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-TITVLILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLG
                        TKSRYYNYAIDWQTGAGCNAAGFFTVFASELSVYTLTVITLERWHTITYAMQLNRKVRLR
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                                        FRGEYNKHAQLWMESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCR
                                                         VLIWFINILAITGNTTVLII--LISSQYKLTVPRFLMCNLAFADLCIGIYLLFIASVDIQ
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Similarity 24.7%;
74; Conservative 1
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EXTRACELLULAR
5 (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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LRR 5.
LRR 6.
LRR 7.
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CYTOPLASMIC (F
4 (POTENTIAL).
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LINKED (GLCNAC...)
-LINKED (GLCNAC...)
-V (IN REF. 2).
-> A (IN REF. 2).
-> A (IN REF. 2).
-> T (IN REF. 2).
-> S (IN REF. 2).
-> S (IN REF. 2).
-> L (IN REF. 2).
-> S (IN REF. 2).
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654

LNVLAFVIICICYICIYFTVRNPNVISS-----NSDTKIAKRMAILIFTDFLCMAPISF 590 INLAAFIIIVFSYGSMEYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFV 611 HAVIIMVFGWMFAFTVALLPI----FGISSYMKVSICLPMHIETPFS---QAY-VIFLLV

RESULT

SHEEP

FSHR_SHEEP

STANDARD; P : Q28574; Q9TSI9;

PRT;

695

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Eukaryota; Metazoa; CHOI Mammalia; Eutheria; Ceta Bovidae; Caprinae; Ovis. NCBI_TaxID=9940;

Ovis aries receptor).

(Sheep).

Chordata;

Yarney T.A., Sairam Seidah N.G.;

MEDLINE=93351750; PubMed=8394255; Yarney T.A., Sairam M.R., Khan H. SEQUENCE FROM N.A. (ISOFORM FSH-R1).

[SSUE=Testis;

536

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Sairam M.R., Subbarayan V.S.R.;

"Characterization of the 5' flanking region and potential control elements of the ovine follitropin receptor gene.";

Mol. Reprod. Dev. 48:480-487(1997)

-!- FUNCTION: Receptor for follicle stimulating hormone. The activity of isoform FSH-R1 is mediated by G proteins which activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P35379; Q28573; Q28574; Q9TSI9;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM FSH-R3), STRAIN-DORSET-LEICESTER SUFFOLK; TIS MEDLINE-20391225; Pubmed-10527886;
                                                                                                                                                                                                                                                                                                                                                  Khan H., Yarney T.A., Sairam M.R.; "Cloning of alternately spliced mRNA transcripts coding for variants of owine testicular follitropin receptor lacking the G protein
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM FSH-R2), AND CHARACTE STRAIN-DORSET-LEICESTER-SUFFOLK 1; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                              coupling domains.";
Biochem. Biophys. Res. Commun. 190:888-894(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                stimulating hormone receptor.";
Mol. Cell. Endocrinol. 93:219-226(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and expression of the
                                                                                                                                     P.S., Jiang L., Sairam A.M., Touyz R.M., Sairam M.R., uctural features and expression of an alternatively spor type I receptor for follitropin signaling in the de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cetartiodactyla;
                                                                                                              2:21-27(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebraı
actyla; Ruminantia;
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                                                                                                                                                                                                                                                                          MacDonald
                                                                                                                                                                                 TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                4 AND FSH-R3).
TISSUE=Testis;
                                                                                                                                                                                                                                                    expression
                                                                                                                                                                                                                                        alteration
                                                                                                                                                                                             AND
   proteins
and FSH-F
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                                                                                                                                                                                             CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovine
                                                                                                                                     alternatively spliced growth gnaling in the developing
                                                                                                                                                                                                                                                                         E.A., Laird D.W.,
   FSH-R3
                                                                                                                                                                                                                                                  of a testicular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        testicular follicle
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  also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Payne
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   bind
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   FSH,
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   VARSPLIC VARSPLIC
                                              DISULFID
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CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                               SMART; SMUUU13; LKKNAI, 1.

PROSITE; PS50237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

G-receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm_1; 1
Pfam; PF00560; LRR; 5.
Pfam; PF01462; LRRNT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC1493; JC1493.
HSSP; P23945; 1XUN.
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IPR001611; LRR.
IPR000372; LRR_Nterm.
                                                                                                                                                           Repeat;
                                   1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                                             N-LINKED
N-LINKED
N-LINKED
LISNIGIK -> FKRWRNRI (IN ISOFORM FSH-R4).
MISSING (IN ISOFORM FSH-R4).
DISRIRIRSLPSYGLENLKKLRAKSTYHLKKLPSLE
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7 (POTENTIAL).
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1 (POTENTIAL).
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TEST AND AREA TO BE TO THE TEST AND AREA TO THE

STRAIN=DORSET-LEICESTER-SUFFOLK 1
MEDLINE=93176195; PubMed=8439338;

SEQUENCE FROM N.A.

(ISOFORMS FSH-R4

1;

follitropin receptor with selective that affects signaling function."; Mol. Reprod. Dev. 48:458-470(1997).

Yarney T.A., Jiang Sairam M.R.;

MEDLINE=98031015; PubMed=9364440;

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Khan н.,

"Molecular cloning, structure,

and

MEDLINE=98031017; PubMed=9364442; Sairam M.R., Subbarayan V.S.R.;

adenylate cyclase. Isoforms

SEQUENCE OF 1-51 FROM N.A.

Biol.

Res.

Commun.

ovary. "Structural

> this does not result in activation of adenylate FSH-R3 may be involved in calcium signaling cyclase. Plasma FSH-R3) membrane Isoform

SUBCELLULAR LOCATION: Integral membrane protein. Plasmu (isoforms FSH-R1 and FSH-R2); Cell surface (isoform FS) ALTERNATIVE PRODUCTS: 4 isoforms; FSH-R1 (shown here). FSH-R2,

FSH-R3 and FSH-R4; are produced by alternative splicing. TISSUE SPECIFICITY: ISOform FSH-R3 is expressed in owary testis, but not in kidney.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED REC and

' SIMILARITY: BELONGS TO FÂMILY 1 OF G-PROTEIN COUPLED FSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR). RECEPTORS

This SWI the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL noved. Usage by and for commercial
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tities requires a license agreement (S send an email to license@isb-sib.ch).

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P35376;
01-JUN-1994
01-JUN-1994
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Follicle sti
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   taurus (Bovine).
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Pred. No. 2.
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MISSING (IN ISOFORM FSH-R3).

KEGCYEVQAGYYRSETSFTAHNFHPRNG ->
CNHESSLFVARGNIFLKILD (IN ISOFORM
MISSING (IN ISOFORM FSH-R2).
                                                receptor precursor
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                                                (FSH-R)
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                                              (Follitropin
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR000377; LRR_Nterm.
Pfam; PP00001; 7tm 1; 1.
Pfam; PF00560; LRR; 5.
Pfam; PF01462; LRRW; 1.
Pfam; PF01462; LRRW; 1.
PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR00137; FSHECEPTOR.
SMART; SM00013; LRRNT; 1.
                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                         REPEAT
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NCBI_TaxID=9913;
                              CARBOHYD
                                                                                                                                                                                                                                                                                                              DOMAIN
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL)
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Matches
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P49059; 077514;
01-FEB-1996 (Rel
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15-DEC-1998 (Rel. 37, Last seq
16-OCT-2001 (Rel. 40, Last anno
Follicle stimulating hormone r
                                                                                                                                                                                                        PIG
                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                  Sus
   MEDLINE=96011644; PubMed=7590277;
Remy J.J., Lahbib-Mansais Y., Yer
                                     SEQUENCE FROM N.A.
                                                             NCBI_TaxID=9823;
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                             [SSUE=Ovary;
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                                                                                                                                                                                            STANDARD;
                                                                                                                              37, Last sequence update)
40, Last annotation update)
ing hormone receptor precursor
                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%; Sci
24.5%; Pr
ative 126;
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Pred. No. 3.7e-23;
6; Mismatches 248;
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TRANSMEM
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la Barbera A.R.;
"Porcine follicle-stimulating hormone receptor.";
"Porcine follicle-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ HAMMONE.
-i- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE.
                                                                                   REPEAT
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REPEAT
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR01143; FSHRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
HSSP;
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"The porcine follitropin receptor: cDNA cloning, functional expression and chromosomal localization of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Ovary;
Wang Y.F., Me
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; AF025377;
; P23945; 1
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IPR001611;
IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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7; AAC24981.1;
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LRR 6.
BY SIMILARITY.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
S -> A (IN REF. 1).
T -> S (IN REF. 1).
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                     WVVIFIL--PINSALNPILYTLTTRPFK
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Endocrinology 138:2481-2490(1997).
-1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMOTHE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS
ACTIVATE ADENVIATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
MEDLINE=97307697; PubMed=9165039;
Zhang F.-P., Rannikko A.S., Manna P.R., Fraser H.M., Huhtaniemi I.T.;
"Cloning and functional expression of the luteinizing hormone
"Cloning and functional expression of the luteinizing hormone
receptor complementary deoxyribonucleic acid from the marmoset monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                    Phosphorylation;
SIGNAL 1
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prosite; ps50262; G_protein_recep_r1_2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00373; GLYCHORMONER. PRINTS; PR01144; LSHRECEPTOR. SMART; SM00013; LRRNT; 1.
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InterPro; IPR0001611; LRR.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCRDb; GCR_1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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996 (Rel. 33, Last sequence update)
001 (Rel. 40, Last annotation updat
stimulating hormone receptor precu
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23.8%;
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Pred. No. 1.6e-
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Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00237; GPCRRHODO
SMART; SM00013; LRRNT; 1.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 201:201-207(1994).

-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE !-

-!- FUNCTION: RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE

ADENYLATE CYCLASE. AMONG ALL MAMMALIAN FSH RECEPTORS, ON 1

RECEPTOR DOES NOT BIND LH/CHORIONIC GONADOTROPHIN (CG).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS SUBCELLULAR SUBGRANILY.
                                                                               REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001611;
InterPro; IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS
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P23945; 1XUN.
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em S., Christophe
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LRR 4.

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BY SIMILARITY.

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N-LINKED (GLCNA)

N-LINKED (GLCNA)
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Best Local Sin
Matches 166;
                                                                 Rattus norvegicus (Ra
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10116;
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01-FEB-1991 (Rel. 1
16-OCT-2001 (Rel. 4
Follicle stimulatir
  SEQUENCE FROM N.A. TISSUE-Sertoli cells; MEDLINE-91125358; Pub
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Pred. No. 2.4e-22;
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GCRDb; GCR_0456; ...
GCRDb; GCR_0456; ...
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 3.
Pfam; PF01462; LRRNT; 1.
PFINTS; PR00373; GLYCHORMONER.
PRINTS; PR001143; FSHRECEPTOR.
SMART; SM00013; LRRNT; 1.
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PIR; A34548; A34548.
PIR; A41729; A41729.
HSSP; P23945; 1XUN.
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                             P16582;
P16582;
O1-AUG-1990 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lutropin-choriogonadotropic hormone receptor
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llarity 22.7%;
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 Euteleostomi;
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   PARTE 
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodp
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
Pfam; PF000001; 7tm_1; 1.
Pfam; PF00560; LRR; 2.
PRINTS; PR00373; GLYCHORMONER.
PRINTS; PR01144; LSHRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M29525; AAA31062.1;
EMBL; M29526; AAA31063.1;
EMBL; M29527; AAA31064.1;
EMBL; M29528; AAAA31065.1;
PIR; A41344; A41344.
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PIR; B41344; B41344.

PIR; C41344; C41344.

PIR; C41344; C41344.

HSSP; P22888; ILUT.

GCRDb; GCR_0106; -.

GCRDb; GCR_0608; -.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89332517; PubMed=2502844; Loosfelt H., Misrahi M., Atger M., Solivet A., Guiochon-Mantel A., Sar Milgrom E.; "Cloning and sequencing of porcine lacking transmembrane domain.";
                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
SIGNAL 1
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NCBI_TaxID=9823;
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ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE)
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COURSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     veen the Swiss Institute of Bioinf
European Bioinformatics Institute
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r S., Jallal
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B., Garnier
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mes 144; Conserv
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                                                                                                                                                                   NYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITAT
                                                                                                                                                                                                                TEVSVLLLTFLTLEKYICIVYÞFRCVRÞGKCR-TITVLILIWITGFIVAFIPLSNKEFFK
                                                                                                                                                                                                                                               KLYAMSII---SLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQLVGSLAILS
                                                                                                                                                                                                                                                                                                                                                                                  SILDISSTKLQALPSYGLESIQTLIATSSYSLKKLPSREKFTNLLDATLTYPSHCC----
                                                                                                                                                                                                                                                                                                                                                                                                         DELDLGSNKIENLPPLIFKDLKEL---SQLNLSYNPIQKIQANQFDYLVKLKSLSLEGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSHNR-ITFLKPGVFEDLHRLEWLIIEDNHLSRISPPT--FYGLNSLILLVLMNNVLTRL
                                                                                         NSALNPILYTLTTRPFK
                                                                                                                               EIRNQVKKEMILAKREFEIVFTDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFIL--PI
                                                                                                                                                                                                   SELSVYTLTVITLERWHTITYAIQLDQKLRLRHAIPIMLGGWLFSTLIAMLPLVG----V
                                                                                                                                                                                                                                                                                             GFC--SPKTLQCAPEPDAFNPCEDIMGYDFLRVLIWLINILAIMGNVTVLFV--LLTSHY
                                                                                                                                                                                                                                                                                                                 -YCGYAPHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVICMRPYIRSEN 402
                                                                                                                                                                                                                                                                                                                                       ----AFRNLPTKEQNFSFSIFKNFSKQCESTARRPNNETLYSAIFAESELSDWDYDY
                                                                                                                                                                                                                                                                                                                                                             ISNIQQRMFRPL----MNLSHIYFKKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                              PANAFQGMNNESITLKLYGNGFEEIQSHAFNGTTLISLELKENAHLKKMHNDAFRGARGP
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                                                                  NSCANPFLYAIFTKAFR
                                                                                                                                                        SSYMKVSICLPM----DVETTLSQVYILTILI-LNVVAFIIICACYIKIYFAVQNPELMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696
                                                                                                              NKDTKIAKKMAVLIFTDFTCMAPISFFAISAALKVPLI-TVTNSKVLLVLFYPV
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            STANDARD;
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78092 MW;
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YSAIFARSELSDW -> 1
ISOFORM B).

MISSING (IN ISOFO)
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Pred. No. 3.7e-22;
3; Mismatches 261;
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LRR
LRR
            PRT;
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DOMAIN
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REPEAT
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
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the Euro
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DOMAIN
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TRANSMEM
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                     EMBL; X74454; CAA52463.1;
PIR; S36452; S36452.
PIR; JN0898; JN0898.
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis."; Biochem. Biophys. Res. Commun. 196:1066-1072(1993).
-I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE.
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                                                                                                                                                                                                            GCRDb; GCR_0653;
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor).
                                                                                                   TRANSMEM
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                               PhosphoryLation;
                                                                                                                                                                                                                          G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.; Molecular cloning of the testicular follicle stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        veen the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED FSH/LSH/TSH SUBFAMILY. SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                     PS00237;
PS50262;
                                                                                                                                                                                                                          coupled
 Repeat;
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                                                                                                                                                                                                                         G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
 ormatics Institute. There are no rest institutions as long as its content
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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2 (POTENTIAL
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Best Loc
Matches
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16-OCT-2001
Follicle sti
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REPEAT
REPEAT
   Eukaryota;
                 Homo sapiens
                                               receptor).
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                                                                                                                                                                                                                                VEIPGTITSWVVIFIL--PINSALNPILYTLTTRPFK 654
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                                                                                                                                                                                                                                                                                                       IVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPIFVVKFLSLLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QESKVTEIPSDLPRNAIELR----FVHTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEAD
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                                                                                                                                                                                                                                                                           ICGCYTHIYLTVRNPNIVSS-----SSDTRIAKRMAMLIFTDFLCMAPISFFAISASLK
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                                                             stimulating
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   Metazoa;
                                                                           (Rel. 21,
(Rel. 29,
(Rel. 40,
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                 (Human)
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1192
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78343
                                                                       21, Created)
29, Last sequence up
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 Chordata;
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                                                             hormone
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BY SIMILARITY.
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                                                          notation update)
receptor precursor
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Pred. No. 4e-22;
 Craniata;
                                                                                                                                       PRT;
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                                                                                          update:
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 Vertebrata;
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                                                            (FSH-R) (Follitropin
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EMBL; M65085; AAA52477.1; -
EMBL; 859900; AAB26480.1; -
EMBL; M95489; AAA52478.1; -
EMBL; X68044; CAA48179.1; -
EMBL; X73199; AAB32071.1; -
PIR; JN0122; JN0122,
PDB; 1XUN; 15-MAY-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural predictions for the ligand-binding region hormone receptors and the nature of hormone-receptor i structure 3:1341-1353(1995).

-i- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMON OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH A
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gromoll J., Dankbar B., Gudermann T.;
"Characterization of the 5' flanking reg
stimulating hormone receptor gene.";
Mol. Cell. Endocrinol. 102:93-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tilly L.T., Aihara T.,
Kowalski K.I., Perlas
Submitted (XXX-1992) t
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Kelton C.A., Cheng S.V., Nugent N.P.
Rosenthal J.L., Overton S.A., Wands
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Hendrickson W.A., el Tayar N.;
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"Molecular cloning of a truncated isoform
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SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS
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sen the Swiss Institute of Bioinformatics
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PubMed=7926278;
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ng of human FSH receptor cDNA.";
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Pfam; PF00560; LRR; 4.
Pfam; PF001462; LRRN; 1.
PAINTS; PR00373; GLYCHORMONER.
PRINTS; PR01143; FSHRECEPTOR.
SMART; SM00013; LRRNT; 1.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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23.1%;
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL).
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6e-22;
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FSHR_MOUSE STANDARD; PRT; 6
AC P35378; Q9QWV8; Q9D4C2;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation
DE Follicle stimulating hormone receptor
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STRAIN-19/SV; TISSUE-Testis;
Pena-Sempere M., Manna P.R., Huhtaniemi I.T.;
"Molecular cloning of the mouse follicle stimulating horn complementary deoxyribonucleic acid: functional expressic alternatively spliced variants and receptor inactivation transition in exon 7 of the coding sequence.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Testis;
medLiNE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Sciurognathi; Muridae;
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MGD; MGI:9583; FShr.
InterPro; IPR000276; LRR_Rhodp.
InterPro; IPR001611; LRR_Nterm.
InterPro; IPR001617; LRR_Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00237; GPCRRHODOPSN.
SMARP; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences and promoter activity.";
Mol. Cell. Endocrinol. 88:55-66(992).
-!- FUNCTION: RECEPTOR FOR FOLLICLE STIM
OF THIS RECEPTOR IS MEDIATED BY G PR
ADENYLATE CYCLASE.
-!- SUBCELLULAR LOCATION: Integral membr
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G
FSH/LSH/TSH SUBFAMILY.
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                                                                                                                                                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
pROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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MEDLINE=93093308;
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Hayashizaki Y.;
Hayashizaki annotation of a
Nature 409:685-690(2001).
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BAB30351.1; -.
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-I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. TOF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIV
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InterPro; IPR000372;
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SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS
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RESULT 14
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ID LSHR_MOUSE STANDARD
AC 930730;
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DT 01-APR-1993 (Rel. 40, L
DT 16-OCT-2001 (Rel. 40, L
DT Lutropin-choriogonadotr
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GN LHCGR OR LHR.
OS Mus musculus (Mouse).
OC Euwaryota; Metazoa; Cho
OC Mammalla; Eutheria; Rod
OX NCBI_TaxID=10090;
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16-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
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                                                           Chordata;
Rodentia;
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EMBL; S49753; AAB24402.1;
EMBL; M81310; AAA39432.1;
EMBL; M87571; AAA39433.1;
PIR; A42395; A42395
HSSP; P22888; 1LUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is provided the EMBL ourself the Ewropean the Swiss Institute of Bioinformatics and the EMBL ourself the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way are by and for commercial there are not removed. Usage by and for commercial content is the statement is not removed. Usage by and for commercial there are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=31993308; PubMed=1459341;
Hubtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel in the murine lutainizing hormone and follicle-stimulating hormone receptor genes: transcription initiation sites, putative promoter sequences and promoter activity ";
Mol. Cell. Endocrinol. 88:55-66(1992).
-i- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gudermann T., Birnbaumer M., Birnbaumer L.;
"Evidence for dual coupling of the murine luteinizing hormone receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+ mobilization. Studies with the cloned murine luteinizing hormone receptor expressed in L cells.",
J. Biol. Chem. 267:4479-4488(1992).
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GCRDb; GCR_0305; -.
MGD; MGI:96783; Lhcgr.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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Phosphorylation;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled_receptor; Transmembrane; Glycoprotein;
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n; PF00560; LRR; 3.
NTS; PR00373; GLYCHORMONER.
NTS; PR01144; LSHRECEPTOR.
RT; SM00013; LRRNT; 1.
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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Matches 148
Eukaryota; Metazoa; (Mammalia; Eutheria; )
NCBI_TaxID=10116;
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01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lutropin choriogonadotropic hormone receptor
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18; Conservative
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SEQUENCE OF 295-700 FROM N.A.
WEDLINE=91060531; PubMed=2174034;
Tsai-Morris C.H., Buczko E., Wang W., Dufau M.L.;
"Intronic nature of the rat luteinizing hormone rec a soluble receptor subspecies with hormone binding J. Biol. Chem. 265:19385-19388(1990).
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MEDILINE-91209270; PubMed-2019252;

KOO Y.B., Slaughter R.G., Ji T.H.;

"Structure of the luteinizing hormone exons of the coding sequence.";

Endocrinology 128:2297-2308(1991).
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"Structure of the lutropin/choriogonadotropin
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MEDLINE-91126285; PubMed-2281186;
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Rosemblit N., Nikolics K., Segaloff D.I
"Lutropin-choriogonadotropin receptor:
protein-coupled receptor family.";
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ACTIVATE ADENVIATE CYCLASE.
SUBCELLULAR LOCATION: Integra
LATERNATIVE PRODUCTS: AT LEAS
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SIMILARITY: BELONGS TO FAMILY
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FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONAL THE ACTIVITY OF THIS RECEPTOR IS MEDIATED IN THE ACTIVITY OF THE ACTIVITY OF THIS RECEPTOR IS MEDIATED IN THE ACTIVITY OF THE ACTIV
                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.
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Search completed: September 5, 2002, 09:04:06 Job time: 2325 sec

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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

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                                   Q91ZZ5 PRELIMINARY; PRT; 737 AA.
Q91ZZ5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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Overbeek P.A., Gorlov I.P., Sutherland R.W., Houston J.B.
Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik
"A transgenic insertion causing cryptorchidism in mice.",
Genesis 30:26-35(2001).
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Rodentia;
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pred. No. 1.2e-133;
18; Mismatches 181;
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Sciurognathi; Muridae; Murinae;
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                                      -EMPPELMKP
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; Murinae; Mus
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RESULT Q9VBP0 ID Q9 AC Q9

Q9VBP0;

PRELIMINARY;

PRT;

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                                                                    Query Match
Best Local Similarity
Matches 132; Conser
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Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X. Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO FAMILY 1 OF EMBL; AE003753; AAF56490.1; -. FlyBase; FBgn0039354; CG5042. InterPro; IPR002106; AA_tRNA_ligase_II.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                       PROSITE; PS00237; PROSITE; PS50262;
                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002106; AA_tRNA_ligas
InterPro; IPR000276; GPCR_Rhodpsn.
                             349
PHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCEGNIFVICMRPYIRSENKLYAMS 408
                                                                                                                                                                                    PR00237; GPCRRHODOPSN.

2; PS00339; AA_TENA_LIGASE_II_2; UNKNOWN_1.

3; PS00237; G_PROTEIN_RECEP_F1_1; 1.

2; PS50262; G_PROTEIN_RECEP_F1_2; 1.

3in coupled receptor; Glycoprotein; Transmembrane.

3in coupled receptor; Glycoprotein; Transmembrane.

359 AA; 40880 MW; 71913BEBD7C9E739 CRC64;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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17,
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X., Smith
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Q95Y16;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.; "cDNA cloning and functional analysis of a novel member of the glycoprotein hormone receptor family from a starfish Asterina pectinifera.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2001) to the EMBL; AB061862; BAB68209.1;
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I-----SNIQQRMFRPLMNLSHI---
                                                       NDISYIPADAFQSLSHLDTLSLSNNTIREIDSQAFAPCTSLQYLDLSNNSFPVLPTAGLQ
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                                                                                                            NKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSLE--
                                                                                                                                                                    NMTGLTSLNLHNNLIEGLPSLS--KCSSLKVLHLGTNKLTSLEGQPFSGLHDLYDLQLLE
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1 (TrEMBLrel. 19, Las
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Asterinidae; l
  -YFKKFQYCGY---
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                                                                                                                                                                                                                                                                                                                                            KPLCQ
                                                                                                               GIE 319
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Best Local S
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.;

mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.;

mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.;

mita M., Nagahama Y.;

pectinifera.";

pectinifera.";
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Echinodermata;
Asteroidea; Valvatacea; Valvatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Asterina pectinifera (Starfish).
                                                                                                                                                                                                                                                                            EMBL; AB061861; BAB68208.1;
                                                                                                                                                                                                                                                                                        Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7594;
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                                                                                                                                                                          193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTTRPFK---EMIHRFWYN--YRQR 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLVFTDFACWAPIAFFSLTAAFGLRLISLDGAKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESIGAQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQS-AITATEIRNQVKKEMILAKRF 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIKHALHLEKRMKLPHAITVMCFGWIFSVTAAVLPLVN----VSHYHRVPVCLPF---DV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTYWASGSVPDYYNWTFDINSESWIDSIFGFGSLSIGSPTYLSGNYSRLLVPHNISCRPK 541
 GNSITSIAHTAFRNLPALRNLVILEVKNLSVFPDLTGTTSLEHLGIERCSLRAIPANFCD
                             NNVLTRL-----
                                                        HLSNLRILHLEHNSIPVVPDHAFAENSHLIE-LILRHNKITHLSAHAFAGLPNLWLLEFL
                                                                                   GLNSLTKLYLSHNRITFLKPGVF-EDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLM 195
                                                                                                                 FQQVPRKAFRNDDLANLRKLHLDSNWIREVPADAFMNLTALHHLNLDHNQLSEVPTAALH
                                                                                                                                             FTSVPSVS-----SNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDLQNNKITSISIYAFR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTTVAKYY-VGSILILNILAFVIIMACYASIYLAIQGSHAWNCNDSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPFMPCMDLFGSWPLRIGVWLVFLLAIIGNAIVIFVIIVSHTKMDVPRFLICNLAFADF 601
                                                                                                                                                                                       Similarity
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25.9%;
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Last annotation update)
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                               -----PD-----
                                                                                                                                                                                        Score 576;
Pred. No. 1
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Asterinidae; Asterina.
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                                                                                                                                                                                                                                                                                                                      a novel member of the a starfish Asterina
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                             --KPLCQ
                                                                                                                                                                           Gaps
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     SMART;
                                                                                                                               Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF274591; AAK00808.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001511; LRR.
InterPro; IPR003591; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Nishi S., Hsu S.Y., Zell K., Hsueh A.J.;

"Characterization of two fly LGR (leucine-rich repeat-containing protein-coupled receptor) proteins homologous to vertebrate glycoprotein hormone receptors: constitutively activation of wild fly LGR1 but not LGR2 in transfected mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
01-DEC-2001
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
                                                     PRINTS; PR00237; GPCRRHODOPSN
                                                                                     Pfam; PF00560;
                                                                                                           Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEUCINE-RICH
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REPEAT-CONTAINING G PROTEIN-COUPLED RECEPTOR
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Best Local :
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InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF000560; LRR; 5.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UN
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DGC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DGC-2001 (TrEMBLrel. 19, Last annotation update)
Q0NADOTROPIN RECEPTOR I.
TGTH-RI.
TGTH-RI.
Dreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Dreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
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Oba Y., Hirai T., Yoshiura Y., Yao Z., Nagahama Y.;

"Tilapia gonadotropin receptor I.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AB041762; BAB16106.1; -.
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                          ILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCRTITVLILI-WITGFIVAFIP---LS
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24.9%;
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    RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlaer P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Celniker S.E., Agbayani A., Chavez C., Chew M., Ciesiolka L., Doyle C.M
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir S., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
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Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of management of the address of the addr
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STRAIN=Y, AND CN BW SP;
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, House, Karpe
, Kalush F., Karpe
"~dira C.D., !
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Rubin G.M.;
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittmann G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhano Q., Zhang T.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
PREMBL, AE003408; AAF44046.1; -.
DR EMBL, AE003408; AAF44046.1; -.
DR EMBL, AE003542; AAF53367.2; -.
DR FlyBase; FBgn0003255; rk.
DR InterPro; IPR003591; LRR_typ.
PR Fam; PF00001; 7tm_1; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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VVSAVTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYN
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                                                                 YFEEHDVSGPATGYGFGTGLFSGMSTEDFQPGSVQCLPMPGPFLPCADLFDWWTLRCGVW
                                                                                                                                                                                          AEFDMTLWNNSMMNIWPQMHNLSKQLGASMHDPWETAINFNEEQLQTQTGGQIATSYMEE
                                                                                                                                                                                                                                                                                                                       HLKTFNNPKLREFPPPDTFPRIQTLILSYAYHCCAFLPLVAMSSQKKTSQVQEAVLFPSD
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22.6%;
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Pred. No. 1.9e-
                                                                                                                            --YAPHVRSCKPNTDGISSLENLLASIIQRVFVW
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                                                                                                                                                                                                      Query Match
Best Local S
Matches 182
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 15.
Pfam; PF001462; LRRNT; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P23945; 1XUN.
MGD: MGI:1341817; Gpr49.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003592; LRR_Cut.
InterPro; IPR003591; LRR_Typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Z1P4;
Q9Z1P4;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLREL. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developing mouse.";
Biochem. Biophys. Res. Commun.
EMBL; AF110818; AAD14684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hermey G., Methner A., Schaller H.C., Hermans-Borgmeyer I.; "Identification of a novel seven-transmembrane receptor with 91ycoprotein receptors and its expression in the adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99121227; PubMed=9920770;
Hermey G., Methner A., Schaller H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                   71
                                                                                                                                                                                                      / Match 12.8%;
Local Similarity 24.6%;
nes 182; Conservative 11
                                FVVKFLSLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPFKE
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HHIADYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEF-PTAIKTLS
                                                                                                   SLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTDVPVQAFRSLSALQAMTLALNKI 198
                                                                                                                                                   SLPGLELDWMKPFTSVPSVSSNVTAMSLQW---NLIRKLPPDCFKNYHDLQKLDLQNNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGLQLISLEQAKI-----FTVFVLPLNSCCNPFLYAIMTKQFKK
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                                                                                                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                                                                            LRRNT; 1.
LRR_TYP; 8.
2; G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                                    99681 MW;
                                                                                                                                                                                                         110;
                                                                                                                                                                                                      Score 490; DB 11;
Pred. No. 1.9e-28;
0; Mismatches 263;
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                                                                                                                                                                                                                                                                                                                                 553167C6C0AAE253 CRC64;
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Q9NDI1;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                Eukaryota; Me
Pterygota; Ne
Ephydroidea;
SEQUENCE FROM N.A.

STRAIN-CANTON S.; TISSUE-WHOLE ANIMAL;

MEDLINE-20359836; PubMed=10899142;

Eriksen K.K., Hauser F., Schlott M., Pedersen K.-M., Soendergaa Grimmelikhuijzen C.J.P.;

"Molecular Cloning, Genomic Organization, Developmental Regulat and a Knock-Out Mutant of a Novel Leu-Rich Repeats-Containing G Protein-Coupled Receptor (DLGR-2) from Drosophila melanogaster. Genome Res. 10:924-938 (2000).

EMBL; AP142343; AB66608.1; -.

HSSP; Q57815; 1D3Y.

FlyBase; FBgn0003255; rk.
                                                                                                                                                                                                                                        GLYCOPROTEIN HORMONE RECEPTOR II. RK OR BG:DS00180.13 OR CG8930. Drosophila melanogaster (Fruit fly)
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Neoptera; Endopterygota; Diptera;
2, Drosophilidae; Drosophila.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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Pfam; PF00001; 7tm_1; 1.
Pfam; PF00560; LRR; 14.
PRINTS; PR00237; GPCRHRODOPSN.
SMART; SM00370; LRR; 2.
SMART; SM00369; LRR_TYP; 5.
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InterPro;
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MF-INGCAFLTLMGCYLKMYWAIRGSQAWNT----
                         FLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKREFFIVFTDALCWIP
                                                      SLKQAGYIMSVGWVFALIMALMPLVGVSDYRKF----AVCLPF--ETTTGPASLTYVISL
                                                                                  KCRTITVLILI-WITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAI 548
                                                                                                                DAATLGEFRMFAIPWQMSVLCQLSGFLAVLSSELSVYTLAVITLERNYAITHAIHLNKRL
                                                                                                                                            DLKFRGEYNKHAQLWMESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPG
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Pred. No. 5.6e-28;
6; Mismatches 277;
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Q9PVN9;
01-MAY-2000
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Oba Y., Hirai T., Yoshiura Y., Yoshikuni M., Kawauchi H., Nagahama "The duality of fish gonadotropin receptors: cloning and functional characterization of a second gonadotropin receptor cDNA expressed i the ovary and testis of amago salmon (Oncorhynchus rhodurus)."; the ovary and testis of amago salmon (Oncorhynchus rhodurus)."; Biochem. Biophys. Res. Commun. 265:366-371(1999).
EMBL; AB030012; BAA86898.1; -.
EMBL; AB030012; BAA86898.1; -.
EMBL; AB030012; BAA86898.1; -.
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Oncorhynchus rhodurus (amago).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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pfam; pf0056; LRR; 3.
prints; pr00237; gpcrrhodopsn.
prosite; ps00237; g_profein_recep_f1_1;
prosite; ps50262; g_profein_recep_f1_2;
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SV-ACSPAPDAFNPCEDIMGSAPLRVLIWIISVLALLGNTIVLLVLLGSRAKMTVPRFLM
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Matches 156
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii, Weopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
GONADOTROPIN RECEPTOR II.
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Pfam; PF00560; LRR; 2; 6PCRHODDSN.

PRINTS; PR00237; 6PCRHODDSN.

PROSITE; PS00237; 6PROTEIN_RECEP_F1_1;

PROSITE; PS50262; 6PROTEIN_RECEP_F1_2;
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InterPro; IPR001611; LRR.
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                                                  KIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSL-----EGIE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTTRPFKEMIHRFWYNYRQRKSM-DSKGQKTYAPSF----IWVEMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MILAKREFFIVETDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFIL--PINSALNPILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLMMESTHCQLVGSLAILSTEVSVLLLT
     ALRSLPP--
                                                                                                                                                                                                                 DLPKLEYLSISNTGIAHF---PDFTTISS-----LSPNIILEMADNMEIDIIPANSFQGIT
                                                                                                                                                                                                                                                                    DLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLMNNVLTRLPDKPLCQHMPRLHW----
                                                                                                                                                                                                                                                                                                                           LKRVPSHAFKELINITIIEISQSDCITHIQTHAFLSLYSLAQISVQNINSLRFIEKGAFA 123
                                                                                                                                                                                                                                                                                                                                                                              IRKLPPDCFKNYHDLQKLDL-QNNKITSISIYAFRGLNSLTKLYLSH-NRITFLKPGVFE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCMAQRMAILIFTDFLCMAPISFFALSAALKLPLI-TVSDSKLLLVLFYPINSCANPFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHLSFADLCMGIYLVVIATVDVRTRGLYYNHAISWQTGAGCDIAGFFTVFASELSMFTLT
                                                                                                       EEYVDMNLVRNGFKEIKSHAF-NGTKLNTLVLRDNWYLRNIQEDAFEGATGPTLLDVSST
                                                                                                                                        -LDLEGNHIHNLRNLTFISCSNLTVLVMRKN-KINHLNENTFAPLQKLDELDLGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RDFFLLAARYGLFTTKAQVYRTESFSVQQAAWIQMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
NGLRHVKFLKASHAYALKSLPLLESLAELLEAELTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 481; DB 13;
Pred. No. 6.6e-28;
8; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yao Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C3BBEFD8ECFC8988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 104;
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RESULT
Q9DGF5
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                          Query Match
Best Local S
Matches 165
                                                                                                 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DGF5 PRELIMINARY; PRT; 696 AA.
Q9DGF5;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FOLLICLE-STIMULATING HORMONE RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                              Signal; Receptor.
SIGNAL 1
                                                                                                                                                     SMART; SM00013; LRRNT; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                 pfam; pF00001; 7tm_1; 1.
pfam; pF00560; LRR; 4.
prinTs; pR00237; GPCRHODOPSN.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                  HSSP; P23945; 1XUN
                                                                                                                                                                                                                                                                                                   EMBL; AB005587;
                                                                                                                                                                                                                                                                                                              Cynops pyrrhogaster.";
Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                         of a follicle-stimulating hormone
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20403884; PubMed=10944452;
Nakayama Y., Yamamoto T., Oba Y., Nagahama Y., Abe
"Molecular cloning, functional characterization, ar
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8330;
                                                                                                                                                                                                                                           InterPro; IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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32 FPCGNITKCLPQLLHCNGVDDCGNQADEDNCVVVLCQCMSLPGLELDWMKPFTSVP-SVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TK----IAKRMAVLIFTDFLCMAPISFFAISAALRMPLI-TVSHSKILLILFYPINSLCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SII--SLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQLVGSLAILSTEVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APHVRSCKPNTDGISSLENLLASIIQRVFVWVVSAVTCFGNIFVICMRPYIRSENKLYAM
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                                          Similarity
                                                                                                 696
                             Conservative
                                                                                                               18
                                                                                                  AA;
                                                                                                                                                                                                                                                                                                s. Res. Commun.
BAB13501.1; -.
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696
78633
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                                          12.5%;
23.7%;
                                                                                                                                                                                                                                        LRR_Nterm
                                                                                                 MW;
                             133;
                                         Score 479.5;
Pred. No. 8.
                                                                                               POTENTIAL.
POTENTIAL.
; 179A6FC800B71E57
                                                                                                                                                                                                                                                                                                                275:121-128(2000)
                             Mismatches
                                                                                                                                                                                                                                                                                                                                          receptor in the
                          1.6e-28;
1es 250;
                                                                                                                                                                       UNKNOWN_1
                                                      DB 13;
                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                         be S.-I.;
and gene
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                           Indels 149;
                                                      Length
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                                                       696;
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                          Gaps
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RESULT QPPMIC OCCUPANT OCCUPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PW16;
Q9PW16;
Q1-MAY-2000
                              Bogerd J., Andersson E., Blomenrohr M., Tensen C.P., Gran Schulz R.W., Goos H.J.;
"Cloning and functional characterization of a testicular stimulating hormone receptor of the African catfish.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; A0012647; CABS1907.1;
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                 Clarias gariepinus (Sharptooth catfish)
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Siluriformes; Clariidae; Clarias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
FOLLICLE-STIMULATING HORMONE RECEPTOR PRECURSOR.
                                                                                                                                                                                                                           TISSUE=TESTIS;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=13013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
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145; 1XUN.
1PR000276; GPCR_Rhodpsn.
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Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
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Best Local
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Q9VYG0;
Q1-MAY-2000 (TrE
Q1-MAY-2000 (TrE
Q1-JUN-2001 (TrE
CG4187 PROTEIN.
CG4187.
Eukaryota;
Pterygota;
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SEQUENCE
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Pfam; PF00500; LRR; 4.

PRINTS; PR00337; GPCRRHODDSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2;

SIGNAL 22 POTENTIAL.
                           Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                      TEIRNQVKKEMILAKRFFFIVFTDALCWIPI-FVVKFLSLLQVEIPGTITSWVVIFILPI
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                                                                                                                                                                                                                                                                                                                              ELSVYTLTAITLERWHTITYAMRLER--ECRLHHACCVMAFGWVFSVLAALMPVIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCGYAPHVRSCKPNTDGISSLENLLASIIORVFVWVVSAVTCFGNIFVICMRPYIRSENK
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 Metazoa; I Neoptera;
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O (TrEMBLrel. 13,
I (TrEMBLrel. 17,
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                                                                                                                 PRELIMINARY;
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  Endopterygota;
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Last
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Pred. No. 1.1e<sup>•</sup>
94; Mismatches
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FOLLICLE-STIMULATING HORM
5CB49EDDBBD1D4F5 CRC64;
                                                                                                                  PRT;
               Tracheata;
                                                               sequence update) annotation updat
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ismatches 257;
   Diptera;
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               Hexapoda;
                                                                update)
     Brachycera;
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                Insecta;
     Muscomorpha;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS01067; SECE_SEC61G; UNKNOWN_1.

SEQUENCE 334 AA; 37020 MW; 1662F2D467534061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000).
EMBL; AE003491; AAF48237.1; -
FlyBase; FBgn0030458; CG4187.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR_Rhodpsn
InterPro; IPR001901; SecE.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                     LIWITGFIVAFIP-LSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAF 557
                                                                                                                                                                                                                                                                                                                                             KHAQLWMESTHCQLVGSLAILSTEVSVLLLTFLTLEKYICIVYPFRCVRPGKCRTITVLI 498
                                                                                                                                                                                                                                                                                                 KYEETWRHSGVCAFAGFLSTFSCQSSTLLLTLVTWDRLMSVTRPLKPRDTEKVRIVLRLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 477.5; DB 5; 36.1%; Pred. No. 5.2e-28; tive 59; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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- 밁 180 IFILFSYIRMLQAIRDSGGGMRST----HSGRENVVATRFAIIVTTDCACWLPIIVVKLA 235
- Qy SLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPFKEMIHRF :| || : :|: :||:||||||:||||| ||: :|: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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